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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
       SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_vertebrate:
13: sp_vertebrate:
14: sp_unclassifie
15: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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2529
1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
sp_mho:*
sp_mhoge:*
sp_organelle:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
sp_urlassified:*
sp_vrirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                             sp_invertebrate:*
sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	æ	7	6	S	4	ω	2	1	Result No.
240	240.5	245	252	252.5	253	254	254.5	254.5	257	257.5	272	274.5	274.5	397.5	1154	Score
9.5	9.5	9.7	10.0	10.0	10.0	10.0	10.1	10.1	10.2	10.2	10.8	10.9	10.9	15.7	45.6	Query Match
188	434	233	258	258	253	523	258	255	371	497	415	489	489	156	334	Query Match Length DB
11	11	4	11	13	4	13	4	11	4	4	4	11	11	4	6	DB
Q9Z0U6	Q9D2R3	Q96L06	Q99MM7	Q98ST6	Q9H3Y0	Q98ST5	043692	Q9CWG1	Q96K61	09н0в8	Q8TCB8	Q9ET66	Q9JJ56	Q96нн2	Q9BE36	ID
Q9z0u6 rattus norv	Q9d2r3 mus musculu	Q96106 homo sapien	Q99mm7 mus musculu	Q98st6 gallus gall	Q9h3y0 homo sapien	Q98st5 gallus gall	O43692 homo sapien	Q9cwg1 mus musculu	Q96k61 homo sapien	Q9h0b8 homo sapien	Q8tcb8 homo sapien	Q9et66 mus musculu	Q9jj56 mus musculu	Q96hh2 homo sapien	Q9be36 macaca fasc	Description

41 42 43 45	38 39 40	33333	32 32 32	225 225 27 27	17 18 19 20 21
184.5 184.5 184 183 181.5	189.5 189 185.5 185	196.5 196.5 195.5	207 - 5 207 205 203 201 - 5	225 225 219 208	239 235.5 234 231 228.5 226.5
7.3 7.3 7.2	7.5	7.8	8.0 8.0 8.0		9.00 9.00 9.00 9.00
567 1140 162 199 177	1456 207 212 168	380 392 315	244 244 1321 663 250	236 332 217 415 243	203 500 507 266 301 1290
10 13 10	10	บบ40	15 4 11	11 5 6 11	
Q8WUL3 Q96KG7 Q96344 Q8UW25 Q8UW25	Q61830 Q20608 Q20609 Q40397	Q9VFY2 Q960R5 Q9UPK6 Q9XSD3	Q9RIL4 Q91XA3 Q14594 Q44247 Q44247	Q9DAG6 Q9CQ35 077719 044228 088205	Q9H108 Q9H336 Q99MM6 Q969K2 Q95QF6 Q95QF6
Q8wul3 homo Q96kg7 homo Q96344 bras Q8uw25 lapo Q65157 caps	. 7 , , , ,	Q9vfy2 drosc Q960r5 drosc Q9upk6 homo Q9xsd3 macaa	Q91x14 rattus norv Q91xa3 mus musculu Q14594 homo sapien Q44247 hemicentrot Q9d259 mus musculu		omo nus nus nenc
homo sapien homo sapien brassica na lapemis har capsicum an	mus musculu caenorhabdi caenorhabdi nicotiana g	drosophila drosophila homo sapien macaca mula	mus musculu homo sapien hemicentrot mus musculu	mus musculu mus musculu equus cabal halocynthia rattus norv	homo sapien homo sapien mus musculu homo sapien caenorhabdi gallus gall

ALIGNMENTS

Query Match 45.6%; Score 1154; DB 6; Length 334; Best Local Similarity 94.2%; Pred. No. 3.6e-102; Matches 212; Conservative 2; Mismatches 11; Indels 0; G 94 1 MILHPETSPGRCHLLAVILALLGTTWAEVWPPQLQEQAPMAGALNRKESFILLSLHNRLRS 11	9BB36; 9BE36; 9BE36; 1-JUN-2001 (TTEMBLrel. 17, Created) 1-JUN-2001 (TTEMBLrel. 17, Last sequence update) 1-JUN-2002 (TTEMBLrel. 21, Last annotation update) 1-JUN-2002 (TTEMBLrel. 21, Last annotation update) ypothetical 35.9 kDa protein. acaca fascicularis (Crab eating macaque) (Cynomolgu ukaryota; Metazoa; Chordata; Craniata; Vertebrata; ammalia; Eutheria; Primates; Catarrhini; Cercopithe cropithecinae; Macaca. CEL_TaxID=9541; 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 Q9BE36
Length 334; Indels 0; Gaps 0; NRKESFILISLHNRLRS 60	ate) ate) nolgus monkey). ata; Euteleostomi; bithecidae; c., Hirai M., Terao K., que brain cDNA atabases.	

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Best Local
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gene.";
Submitted (JUL-2000) to the ENBL; AB046537; BAB03398.1; -
HSSP; P04284; ICFE.
MGD; MGI:1921366; 1200009H11F
                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cysteine-rich protease inhibitor.
1200009H1RIK OR CRIPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96HH2 PRELIMINARY; PRT; 156 AA. Q96HH2; Q1-DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-DEC-2002 (TrEMBLrel. 20, Last annotation update) Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Unknown (Protein for IMAGE:4178394) (Fragment).
                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PROSITE;
                                                                     Jang J.S., Hahn Y., Chung J.H.;
"Identification of novel mouse cycteine-rich protease inhibitor
                                                                                     Jang J.S., Hahn Y.
                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                          Q9JJ56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008616; AAH08616.1; -. InterPro; IPRO01304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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PF 500615; C_TYPE_LECTIN_1; UNKNOWN_1.
FF; PS50041; C_TYPE_LECTIN_2; l.
ER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AA;
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17134 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      15.7%;
86.9%;
                                                EMBL/GenBank/DDBJ databases
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                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                      Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Best Local
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                                                                                                                                                                                                                              HSSP; P04284; ÎCFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9ET66;
O1-MAR-2001 (TrEMBLrel. 16, Creaton MAR-2001 (TrEMBLrel. 16, Last of Cysteine-rich protease inhibitor.
                                                                                                                                                                                                     Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Jang J.S., Hahn Y., Chung J.H.;
"Genomic structure of murine cysteine-rich protease inhibitor gene.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046539; BAB03453.1; -...
EMBL; AB046538; BAB03453.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0837; V5TPXLIKE.

ProDom; PD000542; Allign_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Pfam; PF00188; SCP; 1.
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                                                                                              13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL
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                                                                  LLLLLIATGPT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV-----EV 123
   RWDDELAAFAKAYAQKC---
                                DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV-----EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGNWHEEHEYYNESTATCDPNQMCGHYTQVVWSKTERIGCGSHFCETLQGVEEANIHLLV 155
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75; Conserv
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                                                                                                                                                                                                     489 AA;
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                                                                                                                                    Conservative
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                                                                                                                                                                                                                                SCP_AG5_PR1_SC7_1; 1.
SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                 52664 MW; 01C2009712E3C76D CRC64;
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                                                                                                                                                 10.9%; Score 274.5; DB 11; Length 32.3%; Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16, Created)16, Last sequence update)21, Last annotation update)
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                                                               ----TALTEDEKQTMVDLHNQYRAQVSPPASDMLQM 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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   -VW----
                                                                                                                                  Mismatches
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-GHNKERGRRGENLFAITDEGMDVPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
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                                                                                                                                                                                                                 DKFZP434B044.

DKFZP434B044.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TCB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 45.2 kDa protein (Fragment).
Hymon sapiens (Human).
Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (JUI-2001) to the EMBI/GenBank/DDBJ databases. EMBI, AL13661; CAB66795.1; -. HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                  09H0B8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 55.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC022399; AAH22399.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09н0в8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                    TISSUE-TESTIS;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LLAVILALIGTTWAEVWPPQLQEQAPMAGALNRKESFILLSLHNRLRSWVQPPAADMRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNYEPPGN--VKGRK--PYQEGTPCSQCPLGYS-C----ENSLCEPMRNP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-----GYHCKNSLCEPIGSP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV-----EV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGNWHEEHEYYNFSTATCDPNQMCGHYTQVVWSKTERIGCGSHFCETLQGVEEANIHLLV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLPLLLLVATT ------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWDEELAAFAKAYARQC-----VW----GHNKERGRRGENLFAITDEGMDVPLA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 AA; 45230 MW; 945069C1607D38E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 272; DB 4; 31.9%; Pred. No. 1.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Mismatches
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RESULT
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Best Local
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InterPro; IPR004043; LCCL_dom.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SMART; SM00198; SCP, AG5_PR1_SC7_2; 1.
Hypothetical protein.
SEQUENCE 497 AA; 55919 MW; 1E7ADDCAB3
InterPro; 150,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,000 | 100,00
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14489 fis, clone MAMMA1002881, weakly similar to
                                                                                                                                                                                                                                                                                                         TISSUE-MAMMARY GLAND;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
"Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027395; BAB55081.1; -.
InterPro; IPR001283; Allrgn_V5/Tpx1.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIPREDKEEILMLHNKLRGQVQPQASNMEYMTWDDELEKSAAAWASQCIWEHG-PT-SLL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTSAVNYMTQVVRCDTKMKDRCKGSTCNRYQCPAGCLNHKAKIFGTL----FYESSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCSECPPSYGGSCRNNLCYREETYTPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPK 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICRAAIHYGILDDKGGLVDITRNGKVPFFVKSERHGVQSLSKYKPSSSFMVSKVKVQDLD
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38; Pred. No. 4.8e-16;
45; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 AA.
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peoole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peosle G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Ra Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CWG1;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AK010768; BAB27168.1; -.
EMBL; BC025083; AAH25083.1; -.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUE-EMBRYONIC STEM CELLS; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
24.10114014Rik protein (RIKEN cDNA 2410114014 gene).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 VSIGQNLGAHWGRYRSPG-----FHVQSWYDEVKDYTYPYPSECNPWCPERCSGPMCTH
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                                                                                                                                                             409:685-690(2001).
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RESULT 9
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                                                                                                                                                                                                                                                                                                                     InterPro; 18,000-18; SCP; 1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_MW; 1915A5831637795F CRC64;
PROSITE; PS01010; SCP_AG5_MW; 1915A5831637795F CRC64;
PROSITE; PS01010; SCP_AG5_MW; 1915A5831637795F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               043692;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D45027; BAA25066.1; -. HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1395:202-208(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenesis-related proteins, and its frequent
brain cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1920940; 2410114014Rik.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PrODOm; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamakawa T., Miyata S., Ogawa N., Koshikawa N., Yasumitsu H.,
Kanamori T., Miyazaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cDNA cloning of a novel trypsin inhibitor with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98146272; PubMed=9473672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 kDa trypsin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01009;
112 HGPSYLLRFL--GQNLSVRTGRYRSILQLVKPWYDEVKDYAFPYPQDCNPRCPMRCFGPM 169
                                                           102 -----RTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGE-----CARNA---T 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106
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                                                                                                                                                                                     43 LNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW- 101
                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 LAVILALIGTTWAEVWPPQLQEQAPMAGAIN------RKESFL--LISIHNRIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                         ISQNDMIAILDYHNQVRGKVFPPAANMEYMVWDENLAKSAEAWAATC-----IWD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSVSSAISAWYEEIKHYDFSTRKCRH--VCGHYTQVVWADSYKLGCAVQLCPNGAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKVSPPARNMLYMSWDPKLAQIAKAWTKSCEFKHNPQLHSRIHPNFTALGENIWLGSLSI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWVQPPAADMRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTL-QVGWNMQLLPAGL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQVILAVI-----VW------MASSVSSSSFTASTLPDITNEDFIKECVQVHNQLR 45
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                          Conservative
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29128 MW; A836ECCB3BACD20A CRC64;
                                                                                                                                                                                                                                                                              10.1%; Score 254.5; DB 4 29.2%; Pred. No. 3.9e-16;
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31.0%;
                                                                                                                                                                                                                                                33; Mismatches
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RESULT Q98757 OF REAL 
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Best Local
  Q9H3Y0;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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Smith D.M., Collins-Racie L.A., Lavallie E.R., Gamer L., Roberts E Marigo V.A., Copeland N.G., Jenkins N.A., McCoy J., Tabin C.J.;

"A novel cysteine-rich secreted protein (CRISP) family member,

"OccoaCrisp, provides insight into the process of septation in the developing chicken midbrain.";
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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ProDom; PD000542; Alirgn_V5/Tpx1; 1.

SMART; SM00198; SCC; 1.

PROSITE; PS01010; SCCP_AG5_PR1_SC7_2; 1.

SEQUENCE 523 AA; 59049 MW; 3AF283C19DC3C55F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF329199; AAK16497.1; -. HSSP; P04284; ICFE. InterPro; IPR001283; Allrgn_V5/Tpx1. InterPro; IPR004043; LCCL_dom. Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98ST5
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                                                                                                                    Q9H3Y0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGVPCSSCPPSYGG----
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                                                                                                                                                                                                                                                              GSEDSEKNEVISTQQMSQIVSCEVRLRDQCKGTTCNRYECPAGC 330
                                                                                                                                                                                                                                                                                                                    GR-----YCQVRCSLQCVHGRFREEECSCVC 282
                                                                                                                                                                                                                                                                                                                                                                             GGCRENLCYREGS-----ERPYSPHEPEEETNEIERQRSKAQDATAQSRPRTHSPSGST
                                                                                                                                                                                                                                                                                                                                                                                                                                     G-----RMSCQNHGRLNISTCHCHCPPGYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQLGCGRHLCSA----GQTAIEA--FVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HWGRYRPP-----TFHVQAWYDEVRDFTYPHPHECNPYCPYKCSGPVCTHYTQVVWATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWNMQLLPAGLASFVEVVSLWFAEGQRYSHA-AGEC-----ARNATCTHYTQLVWATS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILDLHNKLRGQVYPPASNMEYMTWDTELERSAESWAETCLWEHG--PASLLPSIGQNLGA 122
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                                                           (TrEMBLrel.
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  (TrEMBLrel.
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                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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RESULT 12
Q98ST6
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                098ST6 PRELIMINARY; PRT;
098ST6:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence of the control of the control
InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PRINTS; PR00837; V5TPX1KE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SugarCrisp.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; pF00188; SCP; 1.
pRINTS; pR000837; V5TPXLIKE.
proDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SEQUENCE 253 AA; 28605 MW; 28976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL117382; CAC04190.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt DJ881L22.3} (novel protein similar to a trypsin inhibitor). {\tt DJ881L22.3}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        chicken embryo.";

Mech. Dev. 102:223-226(2001).

EMBL; AF329195; AAK16493.1; -.

HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                         Tabin C.J.; "Cloning and expression of a novel cysteine-rich secreted present member expressed in thyroid and pancreatic mesoderm
                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.M., Collins-Racie L.A., Marigo V.A., Roberts D.J., Hartmann C., Schweitzer R., LaVallie E.R., Gamer L., McCoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=STAGE 26 LIMB BUD; MEDLINE=21184121; PubMed=11287197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LLSCHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWR-----TL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVGWNMQLLPAGLASFVEVVSLWFAEGQRY-----SHAAGECARNATCTHYTQLVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLDYHNHIRASVYPPAANMEYMVWDKRLARAAEAWATQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYQGSCNSNMCFK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSG-----CFK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSNRLGCAIHTCSSISVWGNTWHRAAYLVCNYAIKGNW--IGES--PYKMGKPCSSCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATSSQLGCGRHLCSA----GQTAIEA--FVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVGQNLSIHSGQYRSVVDLMKSWSEEKWHYLFPAPRDCNPHCPWRC-DGPTCSHYTQMVW
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67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 253; DE 34.7%; Pred. No. 5.36 tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28976C6F32E3887E CRC64;
                                                                                                                                                                                                                                                                                                                                                          cysteine-rich secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
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es 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                               within
                                                                                                                                                                                                                                                                                                                                                                                                                Davis N.M.,
J.,
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ADD DE RETERMENT DE RESERVANTE DE RESERVANTE
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Best Local 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1934659; P115.
InterPro: IPRO01283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1
SEQUENCE 258 AA; 29150 MW; 2FA994A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family member expressed chicken embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and expression of a novel cysteine-rich secreted protein family member expressed in thyroid and pancreatic mesoderm within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabin C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.M., Collins-Racie L.A., Marigo V.A., Roberts D.J., Davis N.M., Hartmann C., Schweitzer R., LaVallie E.R., Gamer L., McCoy J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=21184121; PubMed=11287197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99MM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99MM7
                                                                                                                                                                                                                           112
                             200 KGAWCSLCTASVSG-----CF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 VGVPCSACPPSYGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 KGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 HGPSYLLRFL--GQNLSVRTGRYRSILQLVKPWYDEVKDYAFPYPQDCNPRCPMRCYGPM 169
                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                      43 LNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 LNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                     CTHYTQMVWATSNRIGCAIHTCQNMNVWGSVWRRAV-YLVCNYAPKGNW--IGEA--PYK
                                                                                                                                                   CTHYTQLVWATSSQLGCGRHLC-----SAGQTAIEAFVCAYSPGGNWEVNGKTIIPYK 199
                                                                                                                                                                                                              HGPSYLLRFL--GQNLSVRTGRYRSILQLVKPWYDEVKDYAFPYPQDCNPRCPMRCFGPM 169
                                                                                                                                                                                                                                                                            -----RTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGE-----CARNA---T 146
                                                                                                                                                                                                                                                                                                                                           ISQNDMIAILDYHNQVRGKVFPPAANMEYMVWDENLAKSAEAWAATC-----IWD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHYTQLVWATSSQLGCGRHLC-----SAGQTAIEAFVCAYSPGGNWEVNGKTIIPYK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHA-AGEC-----ARNAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHYTQMVWATSNRIGCAIHTCQNMNVWGSVWRRAV-YLVCNYAPKGNW--IGEA--PYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISQNDMIAILDYHNQVRGKVFPPASNMEYMVWDETLAKSAEAWAATC-----IWD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. 102:223-226(2001).
AF329196; AAK16494.1; -
P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 252; DB 11;
Pred. No. 6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleosto Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2FA994A9A2562640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SCTDN-------LCFPGVTSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                          000 AC 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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ŚEQUENCE FROM N.A.

ŚTRAIN-C57BL/6J; TISSUB-PANCREAS;

MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda .

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka

Aizawa K., Izawa M., Nishi K., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                      1810049824RIK.
1810049824RIK.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9D2R3
Q9D2R3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96L06;
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PROSITE; PS00238; OPSIN; UNKNOWN_1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.
PROSITE; PS01101; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
SEQUENCE 233 AA; 26118 MW; C6BDD48BDB5B91D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC014603; AAH14603.1; ... InterPro; IPR001283; AlTrgn_V5/Tpx1. InterPro; IPR001760; Opsin. Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1700011E04 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                         1810049K24Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 CKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 AMCPNLGGASTAIFVCNYGPAGNF----ANMPPYVRGESCSLCSKE-EKCVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 HLC-SAGQTAIEAFVCAYSPGGNWEYNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 WNMQLLPAGLASFY--EVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 VGVPCSSCPPSYGGACTDNLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 LSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTL----QVG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEVP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENIWL--GGIKSFTPRHAITAWYNETQFYDFDSLSCSR--VCGHYTQLVWANSFYVGCAV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEÄHNEWRGKVNPPAADMKYMIWDKGLAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Search completed: December 29, 2002, 02:25:36 Job time : 94 secs
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0837; V5TPXLIKE.

ProDom; PD000542; Alirgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 434 AA; 48593 MW; C25067E814647AC0 CRC64;
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Nature 409:885-690(2001).
EMBL; AK019034; BAB31519.1; -.
HSSP; P04284; ICFE.
MGD; MGI:1926142; 1810049K24Rik.
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InterPro; IPR004043; LCCL_dom.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 VWATTNKIGCAVHTCRNMNVWGDTWENAVYLVCNYSPKGNW--IGEA--PYKHGRPCSEC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 RTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHA-AGEC-----ARNATCTHYTQL 153
                                                                                                                                                                                    270 RAAIHYG 276
                                                                                                                                                                                                                                                                            281 VCDIGYG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 VWATSSQLGCGRHLCSA----GQTAIEA--FVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.0 nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 QNLAVHWGRYRSPG-----FHVQSWYDEVKDYTYPYPHECTPRCRERCSGPMCTHYTQM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LHNRLRSWYQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW------ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LHNKLRGQVYPPASNMEHWTWDEELERSAAAWAHRC------LWEHGPAGLLRSIG 51
                                                                                                                                                                                                                                                                                                                                                                                                                   PSSYGGGCLNNLCHREKPHKHKPEVDMMNEVESPPAPEETHVWVQPRVIKTKKTPVINFM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TASVSG-----CFKAWDH-----AGGLCEVPRNPC------
                                                                                                                                                                                                                                                                                                                                                                    TQVVHCDTKMKDSCKG-----STCNRYQCPAGCLSNKAKVFGSL-----FYESSSSIC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 240.5; DB 11; Length 434; 28.0%; Pred. No. 1.7e-14; tive 25; Mismatches 91; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 105; Gaps
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       A_Geneseq_101002:*

1: /SIDSZ/gcgdata/ge
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Result	Score	Query Match Length DB	ength		ID .	Description	ption
ب	2529	100.0	455	20	AAY06483	Human	tumour-assoc
2	2529	100.0	455	20	AAY17828	Human	
ω	2529	100.0	455	21	AAY93690	Amino	
4	2447.5	96.8	446	20	AAY41266	. Human	
տ	2447.5	96.8	446	22	AAE06575	Human	
0	2447.5	96.8	446	22	AAB64994	Human	
7	2447.5	96.8	446	23	AAE21077	Human	
8	2426.5	95.9	446	22	AAM93326	Human	
9	2315.5	91.6	420	20	AAY41267	Human	n T139 mature
10	2315.5	91.6	420	23	AAE21078	Human	1139 (TANGO-

18 429.5 19 27.7 20 27.7 21 27.7 22 27.7 23 27.7 24 27.7 25 27.7 26 27.7 27 27.7 28 26.5 31 260.5 31 260.5 32 260.5 33 259.5 34 257.5 35 257.5 36 257.5 37 254.5 41 254.5 42 252.5 43 259.5 44 259.5 45 257.5 46 254.5 47 254.5 48 255.5 48 255.5 49 254.5 40 254.5 41 254.5	. 19
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ABG12158 AABG408 AAM39716 AAM4502 AAM4502 AAY13392 AAV12351 AAX255343 AAU12351 AAB50260 AAW53088 AAW63115 AAB10618 AAB10618 AAB210618 AAB210618 AAB210616 AAB223977 AAB93377 AAB93979 AAE10617 AAB108193979 AAE10819	ABG12157 ABG27603 ABG12156 AAY70015 ABG17023 AAM23810 ABG24318
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                           QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                  DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
                                                                                                                                                                                                                                          TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
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QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS
                                                                                                                                                                                                               TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT
                                                                                                                                                                                                                                                                                                                                                                                                                           AYSPGGNWEYNGKTIIPYKKGAWCSLCTASYSGCFKAWDHAGGLCEVPRNPCRMSCQNHG
                                                                                                    DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL
                                                                                                                                                                                                                                                                                                                      RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
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16-DEC-1997;
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16-DEC-1997;
17-DEC-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                               The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-prolliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 23; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1998;
09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9928462-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 -DEC
                                                                                                                                                                                                                      Local
  61
                                                                                                                  1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
1999-371118/31.
                                               WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
                                                                                            MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
                                                                                                                                                                                             455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO protein; tumour necrosis factor family; TNF ed protein; transmembrane protein; inflammation
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX80053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J,
                                                                                                                                                                                                                                                                                          455 AA;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0069696.
97US-0069702.
97US-0069870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0074086
98US-0074092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0069873
97US-0068017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0075945.
97US-0067411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0070440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0069694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97us-0069335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0069278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard
                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO secreted
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Þ,
                                                                                                                                                                                                                 Score 2529;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane
                                                                                                                                                                                                                 DB 20;
l.7e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF; cytokine;
ion disorder.
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                                             0;
                                                                                                                                                                                             Gaps
  120
                                                                                                 60
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RESULT 3
AAY93690
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WO200037640-A2
                                                                                    Modified-site
                                                                                                         Modified-site
                                                                   Modified-site
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                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                   PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PR0882; tumour cell;
                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of novel polypeptide PRO347
                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93690 standard;
                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                             tumourigenesis; cancer; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEVVSLWFAEGORYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEEECSCVCDIGYGGAQCATKVHFPFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                            /note=
398..4
                                               /note= "1331..337
                                                                                     /note=
287..2
                                                                                                                           213.
                                                                                                                                              /note=
204..2
                                                                                                                                                                 /note=
201..2
                                                                                                                                                                                                                                                        /note=
45..49
                                                                         /note=
                                                                                                                                                                                                          131..137
                                                                                                                                                                                                                            99..105
                                                                                                                                                                                                                                                                           /note= "signal sequence"
22..28
                                                                                                                                                                                      144..148
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 455
                            .404
                                                                                                                                                                  . 207
                                                                                                        . 247
                "N-myristoylation site"
                                   "N-myristoylation site"
                                                                         "N-myristoylation site"
                                                                                            "N-glycosylation site"
                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                                                               "N-myristoylation site"
                                                                                                                                                                                                                                                               "N-myristoylation site"
                                                      "N-myristoylation site"
                                                                                                                "N-myristoylation site"
                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                          "N-glycosylation site"
                                                                                                                                                                                                                                            "CAMP- and cGMP-dependent
                                                                                                                                 "prokaryotic membrane lipoprotein attachment site"
                                                                                                                                                                                                                                   phosphorylation site"
                                                                                                                                                                                                                                                                                                                                           cell proliferation
                                                                                                                                                                                                                                            protein kinase
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> 301 301 361

DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420

DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL

TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT

360

360

TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT

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                                                                                                                                                                                                                                                       QУ
                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                           Matches 455;
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1055, PRO344, PRO347, PRO347, PRO3157, PRO1112, PRO1059, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and prognosis of tumour treatment and diagnosis of neoplastic cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1998;
08-MAR-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                  and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Fig 14; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anti-polypeptide antibody useful in the treatment and neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA46918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-452188/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999
                                 241
                                                            181
                                                                                                                   121
                                                                                                                           121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-2000
                                                                                                                                                                         61
                                                                                                                                                                                                   61
                                                                                                                                                                                                                                      1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
                                                     AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCONHG
RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
                                                                                                                                                                                  WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNWQLLPAGLASF
               RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
                                                                                                           VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC
                                                                                                                                                                   WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
                                                                                                                                                                                                                         MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ď
                                                                                                                                                                                                                                                                                                                                          455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell growth and proliferation
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28409.
99WO-US28301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US12252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US05028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0113296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US30095
                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL,
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                              Score 2529; DB 21;
Pred. No. 1.7e-183;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence DA,
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                        Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                   to contribute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy
                                                                                                                                                                                             120
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                           300
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 300
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RESULT 4
AAY41266
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                                                                                                                                                                           prophylactically to treat/prevent disorders associated with aberrant T139 CC expression or activity, especially proliferative or differentiative CC disorders, e.g. of the immune system. They can be used to modulate CC spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or CC be useful to treat testicular disorders e.g. testicular cancer. The CC polypeptides may be used to identify selectively binding compounds which CC may be useful for detecting the polypeptides in samples; and identifying CC compounds modulating polypeptide activity. The polynucleotides are useful CC polynucleotides which may be useful for detecting the polypeptides to the CC polynucleotides which may be useful for detecting the polynucleotides are useful CC asample, gene mapping; identifying cells or tissues expressing aberrant CC identify subjects at risk for or having a disorder associated with T139 CC expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate CC producing antisense sequences for therapeutic administration to modulate
 В
                                  Ş
                                                                                                          Query Match
                                                                          Matches 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; T139 polypeptide; immune system disorder; spermatogenesis; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY41266 standard; Protein; 446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This represents a human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sperm-egg fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 1; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-633969/54.
N-PSDB; AAZ23299, AAZ23300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holtzman D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                                 Sequence
                                                                                             Local Similarity
QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                                  446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US08896
                                                                                             96.8%;
97.1%;
                                                                          Score 2447.5; DB 20
Pred. No. 2.4e-177;
1; Mismatches 3;
                                                                                                                  DB 20; Length 446;
                                                                                9;
                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                        Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; nultiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic, tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE06575 standard; Protein; 446 AA.
                                                 (PROT-)
                                                                                    06-JAN-2000; 2000JP-0000585.

06-JAN-2000; 2000JP-000588.

11-JAN-2000; 2000JP-0002299.

03-FEB-2000; 2000JP-0026862.

03-MAR-2000; 2000JP-0058367.
                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                               contraceptive;
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                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                 PROTEGENE INC.
SAGAMI CHEM RI
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                                                                                                                                                                                                                                                                                                                                               antiinfertility; antiinflammatory.
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1..27
                                                                                                                                                                                                                                                           28..446
                                                                                                                                                                                                                                                                      /label= Signal_peptide
                                                    RES CENT
                                                                                                                                                                                                                                             "Mature human protein with hydrophobic domain"
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WPI; 2001-418355/44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
             AAB64994 standard; protein; 446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is human protein with hydrophobic domain, HP10760. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
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                                                                                                             QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                                                                                                                                                                                                                                                                                                  TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT
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                                                                                                                                                                                                DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 AA;
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97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (including leukemia), autoimmune diseases, allergies, inflammaterist rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins may be used in the prevention, diagnosis and treatment diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers in the content of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 446-448; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to 26 secreted human proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, diagnosing and/or treating cancers and for promoting
healing -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-2000; 2000WO-US15187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nvolving abnormal angiogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                   61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
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                           TCDLRIDGDCFMVSSEADTYYRARMKCORKGGVLAOIKSOKVQDILAFYLGRLETTNEVT
                                                                                                                                   RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
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TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI
                                                                                                        RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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97.1%;
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XXXX
                                                                                                                                                                                                                                                                                       Human; haematopolesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic; cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer; apoptotic disorder; rheumatoid arthritis; cardiant; renal disorder; rhepatotropic; antipsoriatic; antiallergic; dermatological; virucide; riaq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE21077 standard; Protein; 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human T139 (TANGO-139) protein.
                                                                                                                               29-JUL-1998;
23-APR-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
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                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                  21-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                  23-APR-1998;
22-JUN-1998;
                                                                                                                                                                                           23-APR-1998;
                                                                                                                 29-JUL-1999;
                                              Holtzman DA,
                                                                    (MCCA/)
                                                                                 GOOD/)
                                                                                            (HOLT/) HOLTZMAN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QASAAFNWNNQRCKTRNRYICQFAQEHISRWGPGS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
                      2002-303420/34
                                                                    GOODEARL A
                                                                                                                                                                                                                   2001US-0790264.
                                               Goodearl ADJ,
                                                                                                                                                       98US-0065661.
98US-0102705.
98US-0124538.
                                                                                                                                99US-0298531.
99US-0337930.
                                                                                                                                                                                          98US-0065363.
                                                                                                                     99US-0363630
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232..260
                                                                                                                                                                                                                                                                                                                                                                         /note=
47..19
                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide 27..446
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                     /note= "Epidermal growth factor domain 2"
                                                                                                                                                                                                                                                                                                    264:.291
                                                                                 DJ.
                                                                                                                                                                                                                                                                                                                                                                         .190
                                                                                                                                                                                                                                                                                                                                                   ..412
                                                                                                                                                                                                                                                                                                                                                                                     "Human mature T139 protein"
                                                                                                                                                                                                                                                                                                                                     "C-type
                                                                                                                                                                                                                                                                                                                                                             "Sperm-coating domain"
                                                                                                                                                                                                                                                                                                             "Epidermal growth factor domain 1"
                                                Mccarthy SA;
                                                                                                                                                                                                                                                                                                                                      lectin domain"
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Sequence

446 AA;

DB 23; Length 446;

Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders proliferative disorders

Claim 49; Fig 1; 138pp; English.

cultivouer characterises by their adeliant expression of activity. The cartivodies are useful as modulating agents in regulating a variety of cellular processes e.g. cell proliferation and/or cell differentiation. GC TANGO-139 is useful for treating kidney defects such as kidney failure, rango-125 is useful in wound healing and for treating cancer, TANGO-110 is useful for treating neoplasia. TANGO-177 or WDNM-2 is useful for cerebrovascular disease, and tumours, and injury or trauma cerebratitis, cerebrovascular disease, and tumours, and injury or trauma cerebratic heart disease, cardiovascular disorders, such as ischaemic pancreatitis, cerebrovascular disease, and tumours, and injury or trauma cerebratic heart disease, cardiovascular disorders, such as ischaemic cerebratic place of the state of the state of the endometrial disorders, such as ischaemic cerebratic place of the endometrial disorders, such as ischaemic cerebratic place of the endometrial disorders are useful to treat disorders, hyperplasia of the endometriam. TANGO-110 is useful to treat spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-125 treats prostate disorders, such as inflammatory disorders. TANGO-175, or disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for cereating proliferative disorders, inflammatory disorders. TANGO-175, or wDNM-2 activity also include apoptotic disorders, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, cancer set and apoptotic disorders. The nucleic acids of the invention constraints of the invention disorders and inflammatory disorders of the invention are useful to react are useful to react are useful to react and used in gene therapy. The present sequence is human T139 protein. The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to inhibit a proteinase activity, to modulate cell-cell interactions, haematopoiesis and the ability to modulate clotting. Polypeptide and polynucleotide of the invention are useful for diagnosing and treating disorder characterised by their aberrant expression or activity. The antipolice are useful as modulation are not in requirement a various of

Matches Query Match
Best Local Similarity 301 241 181 181 121 121 1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETINEVT RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 442; TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI Conservative 96.8**%**; 97.1**%**; Score 2447.5; DB 23 Pred. No. 2.4e-177; Prediction 3; Indels 9 Gaps 120 60 60 180 180 120 240 240 1;

DЬ δÃ Вр ΩV DЬ Qy

Q Db Qy D Ωy

Qy 맒

DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH---

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RESULT 8
AAM93326
ID AAM9
XX AAM9
XX AAM9
XX DT 06-N
XX Huma
XX Huma
XX Huma
XX PP 07-J
PR 08-J
PR 02-M
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                                                                                                                                                                                                                                                                                                                                                                   Matches 438;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 2851; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAK94246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-524255/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST
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11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-2000; 2000EP-0114089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide,
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121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
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                                                                                                                              61
                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in genetic manipulation -
                                                       VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
                                                                                                                                                 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
                                                                                                                                                                                                                                                                   MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
                                                                                                                     WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGPWRTLQVGWNMQLLPAGLASF
                                                                                                                                                                                                                                    MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 AA;
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 99JP-0194486.
; 2000JP-0118774.
; 2000JP-0183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        95.9%;
96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pi T, Hayashi K, Is
Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                         Score 2426.5; DB 22;
Pred. No. 9.5e-176;
2; Mismatches 6; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuki
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koga H;
                                                                                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 9
AAY41267
                This is the mature protein sequence of the human T139 polypeptide. The CT T139 polypeptide can be expressed by standard recombinant methodology. CT The T139 cDNA insert is deposited with ATCC under accession number CC 98694. The T139 polypeptides and polynucleotides can be administered CC therapeutically or prophylactically to treat/prevent disorders associated CC with aberrant T139 expression or activity, especially proliferative or CC differentiative disorders, e.g. of the immune system. They can be used to CC modulate spermatogenesis, e.g. as a contraceptive to decrease CC spermatogenesis or to treat disorders related to defects in sperm-egg CC fusion. They may also be useful to treat testicular disorders e.g. CC testicular cancer. The polypeptides may be used to identify selectively conding compounds which may be useful for detecting the polypeptides in CC samples; and identifying compounds modulating polypeptide activity. The CC polynucleotides are useful for producing probes or primers that CC selectively hybridize to the polynucleotides which may be useful for detection the content of the polynucleotides which may be useful for detection the polynucleotides
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     detecting the polynucleotides in a sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 114-115; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ23299, AAZ23300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-633969/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holtzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sperm-egg fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; T139 polypeptide; immune system disorder; spermatogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY41267 standard; Protein; 420 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testicular disorder; testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells or tissues expressing aberrant T139 levels; determining if a gene has been mutated or deleted to identify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate/prevent T139 expression.
                                                                                                                                                                                                                                                                   Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE21078 standard; Protein; 420 AA
                                                                                                                                                                                                        glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-2002 (first entry)
                                                                                                                              systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic; cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer; apoptentic disorder; rheumatoid arthritis; cardiant; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 HISRWGPGS 420
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                                                                                                              nepatotropic; antipsoriatic; antiallergic; dermatological; virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HISRWGPGS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCVHGREREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYYRARMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQFAQE 446
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97.2%;
                                                                                                                                                                                                                                                                                                                                                                   mature protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
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US2002028508-A1

Вb

ALCGIPTPSLASGLWRTLQVGWNWQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNAT

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                                                                                                                                                                                                                                                                                                                                                       contractivity cerebrovascular disease, and tumours, and injury or trauma to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g., cischaemic heart disease, cardiovascular disorders, such as ischaemic heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat crenal (kidney) disorders, such as glomerular disease (e.g., acute and chronic glomerularephritis), TANGO-175 is useful to treat uterine contract the contract of the endometrium. TANGO-110 is useful to treat spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-125 treats prostate disorders, such as inflammatory diseases, Crohn's contracting proliferative disorders, inclammatory disorders. TANGO-175, or CMDNM-2 activity also include apoptotic disorders. TANGO-175, or content in the contract of the contract disorders, e.g., immunodeficiency disorders, viral contents and apoptotic disorders. The nucleic acids of the invention care used in gene therapy. The present sequence is human T139 mature
                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1998;
22-JUN-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to inhibit a proteinase activity, to modulate cell-cell interactions, haematopoiesis and the ability to modulate clotting. Polypeptide and polynucleotide of the invention are useful for diagnosing and treating polynucleotide of the invention are useful for diagnosing and treating disorder characterised by their aberrant expression or activity. The antibodies are useful as modulating agents in regulating a variety of cellular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating kidney defects such as kidney failure, TANGO-125 is useful in wound healing and for treating cancer, TANGO-110 is useful for treating neoplasia, TANGO-17 or WDNM-2 is useful for treating cancer, are useful to treat pancreatic disorders, such as traumed the process of the contraction of the contractio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holtzman DA,
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22-JUN-1999;
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(GOOD/) GOODEARL A D .
(MCCA/) MCCARTHY S A.
                                                                                                                                                                                                                                                                                  Sequence
                                                               EVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARA
                                                                                         EVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARA 86
     ALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNAT 146
                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                          Conservative
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98US-0124538.
99US-0298531.
99US-0337930.
99US-0363630.
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                                                                                                                                                                                                 91.6%;
97.2%;
                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                 Score 2315.5;
Pred. No. 2.3
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                                                                                                                                                                                                       .3e-167;
                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                             Indels
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RESULT 11
ABG12157
ID ABG12
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                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG12157 standard; Protein; 506 AA
(II). (II) is useful for generating antibodies against it, detecting quantitating a polypeptide in tissue, as molecular weight markers and
                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #12148
                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSL
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                                                                                                                                                                                                                                                                           2001-639362/73
                                                                                                                                                   20; SEQ ID No 42516; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
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                                                                                                                                                                                                                                                                                                     RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mapping; gene mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apping; gene therapy;
diagnostic; genetic
molecular weight markers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                forensic;
                                            techniques
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RESULT 12
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ID ABG277
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Best Local S
Matches 369
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG27603 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                              Novel human diagnostic protein #27594.
                                                                                                                                                                                                                                                                                                                                   18-FEB-2002
                                                                                                Homo sapiens
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                                                                                                                                                          supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSPGRGHLLAVLLALLGTT------W--AEVWPPQLQEQAPMAGALNRKESFLLLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLP 114
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                                                                                                                                                                                             chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                     medical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DWSDSLAQLAQARAALCGTPTPSLASGLWRTLQVGWNMQLLP
                                                                                                                                                                 imaging;
                                                                                                                                                              gene mapping; gene
maging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 AA
                                                                                                                                                              genetic (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC Phe invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPCN primers of the production of (II) and gene mapping, and in recombinant production of (II). The CPCN primers of genes are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC trestore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a foot supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 57962; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                        153
333
                                301
                                                                     273
                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                           33 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
                                                                 TCDLRIDGDCFMVSS 347
                                  TCDLRIDGDCFMVSS 315
                                                                                                                                                                                                                                                          VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.5%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>+</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1732; DB 22; Pred. No. 3.4e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                      212
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RESULT 13
ABG12156
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                   Matches
                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG12156 standard; Protein; 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG12156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
  61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
                                                        1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n; chromosome mapping; gene mapping; gene therapy; forensic
supplement; medical imaging; diagnostic; genetic disorder.
                                      MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human diagnostic protein #12147.
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 42515; 103pp; English.
                                                                                                                                                                                                276 AA;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                     45.3%;
93.9%;
                                                                                                                                     Score 1145; DB 22; Pred. No. 6.8e-79;
                                                                                                                   Mismatches
                                                                                                                                                       Length 276;
                                                                                                                   Indels
                                                                                                                   0;
                                                                                                                   Gaps
                                          92
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             The present sequence is that of human protease and associated protein-9 (PPRG-9), which is expressed in urologic and musculoskeletal tissues. It is encoded by cDNA identified in Incyte clone 998626 derived from KINNTUTO1 cDNA library. Anti-PPRG antibodies can be used as therapeutic antagonists, reagents for diagnosis and monitoring diseases and for isolating PPRC. PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring of PPRG-related as probe or primer for diagnosis and monitoring of PPRG-related
                                                                                                                                                                                                                                                                                                Claim 1; Page 84-85; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                       New human proteases, useful for diagnosis, treatment and prevention cell proliferative disorders such as atherosclerosis - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease and associated protein-9; ppRG-9; anti-ppRG antibody; diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorde AIDS; Addison's disease; adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic; hepatototropic; antiinflammatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ50926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protease and associated protein-9 (PPRG-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VEVVSLWFAEGGRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 152
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and gene mapping. PPRG can be used in the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), Hillman JL, Baughn MR, A:
, Yue H, Tang YT, Reddy R,
Lu DAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0119768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Potential Phosphorylation site"
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mature_PPRG-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal_peptide
27..166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guegler KJ;
on C, Au-You
of cell
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9999888
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Best Local
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
                                                                                                                                                                                                                         Claim 20;
                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #17014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG17023 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferative disorders like cancer, arteriosclerosis, atherosclerosis, bursitis, cirrhosis and hepatitis, and immune disorders like AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis and amyloidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNNQLLPAGLASF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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                                                                                                                                                                                                                                                                                                                                                                  2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            supplement; medical imaging; diagnostic; genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                  SEQ ID No 47382; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                   YT;
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Pred. No. 3.2e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Вb ρy В δÃ Дb δÃ DЪ δÃ DЪ οy 88888888888888 δõ Query Match 29.1%; Score 735; DB 22; Best Local Similarity 48.6%; Pred. No. 1.5e-47; Matches 159; Conservative 3; Mismatches 21; disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as for this patent did not appear in the printed appear in Sequence at ftp.wipo.int/pub/published_pct_sequences. 333 LETTNEVIDSDFETRNFWIGREHMGAASAGKRGQKGSWQQTPGSEWANLDYPGPGLTYKT 392 298 PFHTCDLRIDGDCFMVSSEAD-----TYYRAR------353 LETTNEVTDSDFETRNFWI------213 QIKECADEPVGKGYMVSCLVDHRGNITEYQCHQYITKMTAIIFSDYRLICGFMDDCKNDI 272 393 AKDSFRWATGEHQAFTSFAFGQPDNHG 419 AKDSFRWATGEHQAFTSFAFGQPDNHG 404 493 AA; Length 493; Indels 144; Gaps ---GLTYKT 377 324 6;

Search completed: December 29, 2002, 02:23:00 Job time : 82 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compus

Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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2529
1 MLHPETSPGRGHLL
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: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_DBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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109.416 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

5 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	321	Result No.
25529 25529 25529 25529 25529 26447 255229 275229 275229 275229 275229 275229	2529 2529 2529 2529	Score
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Sequence 50, Appl Sequence 47, Appl	Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl	Description

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US-09-944-896-15	US-09-944-403-15	US-09-944-413-15	US-09-870-759-95	US-09-832-320-2	US-09-925-301-930	US-09-925-301-853	US-09-876-225-3	US-10-052-586-70	US-09-999-832A-363	US-09-978-192A-363	US-09-978-697-363	US-09-978-295A-363	US-09-808-602-114	US-09-808-602-112	us-09-808-602-108	US-09-808-602-113	US-09-808-602-109	US-09-808-602-27	US-09-808-602-110	US-09-876-225-2	US-09-909-088B-285	us-09-909-320-285	US-09-902-853-285	US-09-905-291A-285	US-09-790-264-4
15,		Sequence 15, Appl	Sequence 95, Appl	Sequence 2, Appli	Sequence 930, App	Sequence 853, App	Sequence 3, Appli	Sequence 70, Appl	Sequence 363, App	Sequence 363, App	Sequence 363, App			`			Sequence 109, App	Sequence 27, Appl		Sequence 2, Appli	Sequence 285, App	Sequence 285, App	Sequence 285, App	Sequence 285, App	Sequence 4, Appli

ALIGNMENTS

US-09-944-413-50 GENERAL INFORMATION: Sequence 50, Application US/09944413 Patent No. US20020156004A1 APPLICANT: CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3,1997
PRIOR FILING DATE: December 11,1997
PRIOR FILING DATE: December 11,1997 APPLICANT: APPLICANT: PRIOR PRIOR TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 APPLICANT: APPLICANT: Baker, APPLICANT: Botst APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: OR APPLICATION NUMBER: 60/069335
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,278
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,425
OR FILING DATE: December 12, 1997
OR APPLICATION NUMBER: 60/069,696
OR APPLICATION NUMBER: 60/069,696 FILING DATE: APPLICATION NUMBER: 60/069,694 Wood, William Roy, Margaret Tumas, Daniel Godowski, Paul Grimaldi, Christopher Filvaroff, Ellen Hillan, Kenneth Gurney, Austin Goddard, Audrey Gerritsen, Mary Botstein, David Napier, Mary Kljavin, Ivar Eaton, Dan Kevin

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; TYPE: PRT
; ORGANISM: Homo
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                                                 Query Match
Best Local Similarity
Matches 455; Conserv
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LENGTH: 455
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1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US00/08439
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FILING DATE: NO. US20020156004Alember 30,
APPLICATION NUMBER: PCT/US99/28301
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FILING DATE: July 28, 1999
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                                                                      PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
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GENERAL INFORMATION:
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APPLICANT: Wood, William
APPLICATT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
ETLE REFERENCE: P2548P1C1
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APPLICANT:
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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                                    APPLICATION NUMBER: 60/069, FILING DATE: December 16, 1
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Roy, Margaret
Tumas, Daniel
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Grimaldi, Christopher
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DATE:
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                    NUMBER: 60/069,
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; LENGTH: 455
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  1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020165143A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: 60/146, 222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: PCT/US99/28409
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  FILING DATE: December APPLICATION NUMBER: 6
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Grimaldi, Christopher
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PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
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CURRENT FILING DATE: 2001-08-31
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APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: PCT/US01, FILING DATE: February 28, 20
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
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FILING DATE: No. US20020168715A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020168715A1ember 30, 1999
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APPLICATION NUMBER: 60/112,850
FILING DATE: December: 10/112,850
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FILING DATE: February 11, 2000
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: 60/074,09
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,94
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NOS: 120
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NUMBER: PCT/US99/12252
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PRIOR APPLICATION NUMBER: 60/067,411

PRIOR TILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
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                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                 FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
                                                FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
                                                                                         APPLICATION NUMBER: 60/069,696
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Grimaldi,Christopher
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OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MATCh 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
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                  1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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FILING DATE: No. US20020173463A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313 .
FILING DATE: No. US20020173463A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 60/074,092
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CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult I
NUMBER OF SEQ ID NOS: 120
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
FILE REFERENCE: P2548P1C1
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
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                                                                               APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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FILING DATE: December 11, 199
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FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020102647Alember 30,
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
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APPLICATION NUMBER: 60/067,411
PATE: December 3, 1997
                                                                              FILING DATE: December 14, 1997
APPLICATION NUMBER: 60/069,696
APPLICATION NUMBER: 16, 1997
                                                                                                           FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
APPLICATION NUMBER: 61,1997
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APPLICATION NUMBER: 60/069,278
TTTT: December 11, 1997
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5. US20020110859A1
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                                                      NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/074,
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FILLING DATE: NO. US20020110859Alember
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020110859Alember
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US00/14042 FILING DATE: May 22, 2000
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US00/08439 FILING DATE: March 30, 2000
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FILING DATE: MATCh 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US98,
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MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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NUMBER: 60/146,222
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CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: DECEMBER: 60/069, 870
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FILING DATE: July 28,
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FILING DATE: March 3, 199
APPLICATION NUMBER: PCT/US99/12252
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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CURRENT FILING DATE: 2001-09-26
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OR APPLICATION NUMBER: 60/069, 334
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069, 335
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069, 278
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069, 425
OR FILING DATE: December 12, 1997
OR APPLICATION NUMBER: 60/069, 696
OR FILING DATE: December 12, 1997
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                                                                     APPLICATION NUMBER: 60/069,694
FILING DATE: December APPLICATION NUMBER: 60
                                  FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
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61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
                                                                           1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS
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FILING DATE: February 28, 2001
R OF SEQ ID NOS: 120
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
FILING DATE: July 28, 2000
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FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US98/19330
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APPLICANT: Eaton,
APPLICANT: Ferrar
APPLICANT: Filvar
APPLICANT: Gerrit
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CURRENT FILING DATE: 2001-09-26
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
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                                               APPLICATION NUMBER: 60/069,694 FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 60/069,334
FILLING DATE: December 11, 1997
APPLICATION NUMBER: 60/069335
 FILING DATE:
APPLICATION |
                 APPLICATION NUMBER: 60/069,702 FILING DATE: December 16, 1997
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Kljavin, Ivar
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Gerritsen, Mary
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December 16, NUMBER: 60/069
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LENGTH: 45
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61 WYQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGLWRTLQYGWNMQLLPAGLASF
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FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USON
FILING DATE: March 30, 2000
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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FILING DATE: No. US20020132768A1ember 30, 1999
FILING DATE: No. US20020132762
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APPLICATION NUMBER: 60/074,092
FILING DATE: February 0
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APPLICATION NUMBER: PCT/US99/28301
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FILING DATE: March 3, 1999
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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                                                                                                                                                                                                         APPLICATION NUMBER: 60/069335
                                                                       APPLICATION NUMBER: 60/069,425
FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
                                                                                                                                                                                                                                                    FILING DATE: December 3, 1997
APPLICATION NUMBER: 60/069,334
FILING DATE: December 11, 1997
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FILING DATE: December 16, 1
APPLICATION UNMBER: 60/069,
FILING DATE: December 16, 1
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o. US20020132981A1
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                                                                                                                                                                         TYPE: PRT
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OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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FILING DATE: NO. US20020132981Alember 30,
APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: 09/866,028
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PRIOR FILING DATE: December 11, 1997
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PRIOR TILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
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PRIOR APPLICATION NUMBER: 60/069,694
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                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/944,097 CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
                                                   FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
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                                                                                                APPLICATION NUMBER: 60/069,
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Tumas, Daniel
Wood, William
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Hillan, Kenneth
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61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF
                                                                                RAPPLICATION NUMBER: PCT/JUS9/28409
RILING DATE: No. US20020133675Alember 30,
APPLICATION NUMBER: PCT/JUS9/28313
FILING DATE: No. US20020133675Alember 30,
APPLICATION NUMBER: PCT/JUS99/28301
FILING DATE: December1, 1999
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FILING DATE: December 1, 1998
APPLICATION NUMBER: 1, 1998
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APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: March 3,
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 60/075,
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FILING DATE: February 9, 1998
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NUMBER: PCT/US01/06520
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,334
PRIOR APPLICATION NUMBER: 60/069,334
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FILING DATE:
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APPLICATION NUMBER: 60/069,425
FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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                               APPLICATION NUMBER: 60/069, FILING DATE: December 17, 1
                                                                APPLICATION NUMBER: 60/069, FILING DATE: December 16, 1
                                                                                               FILING DATE:
                                                                                                APPLICATION NUMBER: 60/069,694 FILING DATE: December 16, 1997
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Grimaldi, Christopher
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Wood, William
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               NUMBER: 60/069,
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR PELICATION NUMBER: PCT/US99/12252
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020142419Alember 30,
PRIOR FILING DATE: NO. US20020142419Alember 30,
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PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
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PRIOR APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
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FILING DATE: No. US30020142419Alember
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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                                    OR APPLICATION NUMBER: 60/069,696
R FILING DATE: December 16, 1997
PR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,702
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,870
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Gurney,Austin
Hillan,Kenneth
Kljavin,Ivar
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Roy, Margaret
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OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MARCh 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: JUNE 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
Local
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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FILING DATE: No. US20020142958Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: PCT/US99/30095
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CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
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                                                   APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
APPLICATION NUMBER: 60/069,870
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APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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Tumas,Daniel
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Grimaldi, Christopher
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                61 WVQPPAADMRRIDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
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Les 455; Conserv
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APPLICATION NUMBER: PCT/US99/21090
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100.0%; Pred. No. 1.2e-172;
7ative 0; Mismatches 0;
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EMBL; X95240; CAA64527.1; ..

EMBL; X94323; CAA63984.1; ..

HSSP; P04284; 1CFE.

InterPro; IPRO01283; Allrgn_V5/TpX1.

pfam; pF00188; SCP; 1.

pRINTS; PR00837; V5TPXLIKE.

PRODOM; D0000542; Allrgn_V5/TpX1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

Glycoprotein; Signal; Multigene family; Posignal

Polymorphism.

or send an email to license@isb-sib.ch).

##### #		RESI CRS ID AC DT DT	
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ILLE GRAINLES OF Human is-specific gene product ROPHILS, LOCALIZED IN CREAS AND PROSTATE > OUPS MAMMALIAN SCP/TPX1; NUTS PR-1. Produced through a collaboration of the EMBL outstation its and the EMBL outstation its and the EMBL outstation its as its content is in no way Usage by and for commercial http://www.isb-sib.ch/announce/	leostomi o. nn D., y. Prima d CRISP-	(SGP28 protein).	p55068 rattus norv p08299 nicotiana t q08697 lycopersico p16112 homo sapien p35760 vespula mac Q28065 bos taurus Q9um47 homo sapien p35784 vespula ger Q00008 zea mays (m q05110 vespula vul Q27591 drosophila p07053 nicotiana t

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                    autoantigen of guinea pig epididymal spermatozoa.";
Biol. Reprod. 38:423-437(1988).
-I TISSUE SPECIFICITY: TESTIS.
-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                          Foster J.A., Gerton G.L.;

"Autoantigen 1 of the guinea pig sperm acrosome is the homologue mouse Tpx-1 and human TpX1 and is a member of the cysteine-rich secretory protein (CRISP) family.";

Mol. Reprod. Dev. 44:221-229(1996).
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Q60477;
01-NOV-1997
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                                                                                                                                                                                                                                               SEQUENCE OF 22-41.
MEDLINE=88193219; PubMed=3282555;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Hartley; TISSUE=Testis; MEDLINE=96354287; PubMed=9115720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Testis-specific protein TPX-1 precursor (Autoantigen 1) (25 kDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 YEDLYSNCK-----SLKLTLTCKHQLVRDSCKASCNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LLAVLLALLGTTWAEVWP--PQLQEQAPMAGALNRKESFL---LLSLHNRLRSWVQPPAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGNWA--NRLYVPYEQGAPCASCPDNCD------DGLC---TNGCK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQSWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMLKMEWNKEAAANAQKWANQCNYRHSNPKDRMTS----LKCGENLYMSSAS-SSWSQA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQLLPAGLASFVEV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFPVLLFLV----AGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPAR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
239
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 252; DB 1;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE-RICH SECRETORY PROTEIN-3.
N-LINKED (GLCNAC. .) (POTENTIAL)
S -> P (IN DBSNP:495335).
/FTId-VAR_01171B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A -> S (IN DBSNP:1864312).
/FTId=VAR_011719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B4DD79CB7AE9E5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 245,
                                                                                                                                                                                                 y acrosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                            Genomics 28:405-410(1995).
                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                  "Structure and chromosomal localization of the mouse neurocan gene.";
                                                                                                                                                                                                                                  STRAIN=BALB/c; TISSUE=Brain; MEDLINE=96039250; PubMed=749
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                        CSPG3 OR NCAN
                                                                                                                                                                                                                                                                                                                                                                Neurocan core protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00188; SCP; 1.
PFINTS; PR00837; V5TPXLIKE.
PFODOm; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PGCN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U35712; AAC52616.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 LCTNSCEYEDLL--SNCE-------SLKNTAGCEH-QLLVEKCKATC-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 CEDKIY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IINKHNQLRKSVTPPASNMLKMEWSREAAVNAQKWANRCTL-VHSNPDDRKTSTKCGENL
 TISSUE SPECIFICITY: BRAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI ($CR) DOMAIN.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                               DEVELOPMENT BY BINDING TAND N-CAM). CHONDROITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATKVH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQTAIEAFYCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDSLKYYYVCQYCPAGNNVYTKNT--PYKQGIPCASCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YMSSDPSSWSDAIQSWFDESQDFTFGVGPKSHNAVVGHYTQLVWYSSYLVGCGIAYCPN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                 Grimpe B., Kulbe G., Arnold-Ammer I., Beier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                  PubMed=7490074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 TI
; 27248 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                           NEURONAL ADHESION AND NEURITE GROWTH DURING TO NEURAL CELL ADHESION MOLECULES (NG-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
                                                                                                                          SULFATE PROTEOGLYCAN; BINDS TO HYALURONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 240; DB 1
Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TESTIS-SPECIFIC PROTEIN TPX-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58D8DE6EECE16A12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GHCE--NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Loc
Matches
                             Query Match
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PROSITE: PS000022; EGF_1; 3.

PROSITE: PS01186; EGF_2; 1.

PROSITE: PS01187; EGF_CA; 1.

PROSITE: PS01241; LINK; 2.

PROSITE: PS00615; C_TYPE_LECTIN_1; 1.

PROSITE: PS00615; C_TYPE_LECTIN_2; 1.

PROSITE: PS00615; C_TYPE_LECTIN_2; 1.

PROSITE: PS00615; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                           DISULFID
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EGF-like doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                              SEQUENCE
                                                                                                            CARBOHYD
                                                                                                                           CARBOHYD
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                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 om; pD000918; Link; 2. r; SM00032; CCP; 1. r; SM00034; CLECT; 1. sM00179; EGF_CA; 1. sM00001; EGF_like; 1. SM00409; TG: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00059; lectin_c; 1.
PF00084; sushi; 1.
PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001881;
IPR003599;
IPR003006;
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain;
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IPR000561;
                                                                                                                                                                                                                                                  1036
1166
1166
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205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium;
                                                                                          Asx_hydroxyl.
EGF-like.
EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Link.
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              9.3%;
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                                                                137200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Lectin; Sushi; Signal.
                                                                        BY SIMILARITY

BY SIM
   39;
                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE V-TYPE ILINK 1.
LINK 2.
LINK 2.
EGF-LIKE 1.
EGF-LIKE 2, CAIC
C-TYPE LECTIN.
 Pred. No. 2.36
); Mismatches
              Score 236;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEUROCAN CORE PROTEIN
                                                                3014E8E202A2FAEC
   2.3e-11;
ches 119;
                                                                                                                                                                                                                                                                                                                                                                                              CALCIUM-BINDING (POTENTIAL).
                                DB 1;
                               Length 1268;
                                                                CRC64;
    58;
    Gaps
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QY
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           RESULT 4
GLIP_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FACE...
TISSUE=Glial tumor;
MEDLINE-97128816; PubMed-8973356;
MEDLINE-97128816; Purman F., Huynh N., Israel M.A.;
RICH T., Chen P., Furman F., Huynh N., Israel M.A.;
"RTVP-1, a novel human gene with sequence similarity to genes of "RTVP-1, a novel human gene with sequence similarity to genes of spream of the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLIP_HUMAN STANDARD; PRT; 266 AA. P48060; Q15409; Q1-rebs-1996 (Rel. 33, Created) Q1-rov-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 41, Last annotation update) Q1-rov-2002 (Rel. 41, Last annotation update) Q10ma pathogenesis-related protein (G11pr) (RTVP-1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1075
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR,
-GLIOBLASTOMA MULTIFORM/ASTROCYTOMA, BUT NEITHER IN NORMAL FETAL
OR ADULT BRAIN TISSUE, NOR IN OTHER NERVOUS SYSTEM TUMORS.
-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szyperski T., Fernandez C., Mumenthaler C., Wuethrich K.; "Structure comparison of human glioma pathogenesis-related protein GlipR and the plant pathogenesis related protein P14a indicates a functional link between the human immune system and a plant defense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy E.V., Zhang Y., Zhu W., Biggs J.;
"The human glioma pathogenesis related protein is structurally related to plant pathogenesis-related proteins and its gene is expressed specifically in brain tumors.";
Gene 159:131-135(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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Best Local :
   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                 Schambony A., Gentzel M., Wolfes H., Raida M., Neumann
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Perissodactyla; Equidae;
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O19010;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpre; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PRINTS; PR00837; V5TPXLIKE.

ProDom; D0000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

CONFLICT 125 125 D -> N (IN REF. 2).

CONFLICT 209 266 PRODOVKRYYSOVYPGWPIYPRNRYTSLFLIVNSVILILSV

CONFLICT 209 266 PRODOVKRYYSOVYPGWPIYPRNRYTSLFLIVNSVILILSV
                                                                                                                                                                                                                                             Biochim.
                                                                                                                                                                                                                                                            tract
                                                                                                                                                                                                                                                                Toepfer-Petersen E.; "Equine CRISP-3: primary structure and expression in the male genital
                                                                                                                                                                                                                                                                                                                                      TISSUE-Ampull
                                                                                                                                                                                                                                                                                                                       MEDLINE=98422318; PubMed=9748582;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteine-rich secretory protein-3 precursor (CRISP-3).
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                                                                                                                                     AMPULLA AND THE SEMINAL VESICLE.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                    Chim. Biophys. Acta 1387:206-216(1998).
SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED SPECIFIC GRANULES (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE SALIVARY GLAND, IN TH
                                                                      European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
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Pred. No. 1.2e-11
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                         Helothermine precursor (HLTx).
Heloderma horridum horridum (Mexican beaded lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
        Mochca-Morales J., Martin B.M., Possani L.D.;
"Isolation and characterization of helothermine, a novel tox
Heloderma horridum horridum (Mexican beaded lizard) venom.";
Toxicon 28:299-399(1990).
-!- FUNCTION: Toxin that blocks ryanodine receptors. It is tomice; it causes lethargy, partial paralysis of rear limb
                                                                                                                                                                  Morrissette J., Kraetzschmar J., Haendler B., El-Hæ
Mochca-Morales J., Martin B.M., Patel J.R., Moss R.
Schleuning W.-D., Coronado R., Possani L.D.;
"Primary structure and properties of helothermine,
that blocks ryanodine receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                             Q91055;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                              TISSUE=Salivary gland;
MEDLINE=95375162; PubMed=7647234;
                                                                                                           MEDLINE=90260878; PubMed=1693019;
                                                                                                                           TISSUE=Venom;
                                                                                                                                      SEQUENCE OF 20-39, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001283; Allrgn_V5/Tpx1.

Pfam; pF00188; SCP; 1.

PRINTS; PR000837; V5TPXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Multigene family. SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PR0SITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ001400; CAP
HSSP; P04284; ICFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELO_HELHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKE-SFLLLSLHNRLRSWVQPPAADMRR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 LDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWN--MQLLPAGLASFVEVVSLWFA 129
lowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGKTIIPYKKGAWCS-----LCTAS-----VSGCFKAWDHAGGLCEVPRNPCRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCQNHGRL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VN-KINTPYEQGTPCARCPGNCDNGLCTNSCEYEDLVSNCDSLKKIAGCEHELLKENCKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVHDFKYGVGPKTPNAVVGHYTQVVWYSSYRVGCGIAYCPKQGTLKYYYVCQYCPAGNY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQWDSKTATNAQNWANKCLLQHSKAEDRAVGTMKCGENLFMSSIP---NSWSDAIQNWHD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPVLL-FLAAVLLPFFPASGQDPGFAALSITKSEVQKEIVNKHNDLRRTVSPLASNMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
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245 AA;
of body temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 228; DB 1;
Pred. No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE-RICH SECRETORY PROTEIN-3; 893A4E87F402BA22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA
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                                                                                                                                                                                                                                              El-Hayek
              of rear limbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 245;
                                                                                                                                                                                                                                   R.L.,
                                                                         novel toxin
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                                                                                                                                                                                                  a peptide toxin
                         It is toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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Best Local
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pfam; pF00188; SCC; 1.
pRINTS; pR00837; V5TPXLIKE.
proDom; pD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: Produced by the venomous gland.
-:- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FASSE_NEG.
Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
Hypothetical 35.0 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U13619; AAC59730.1; -
                               Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1:
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                             NCBI_TaxID=6239
                                                                                                                                                                                 Rhabditidae;
                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                        YR81_CAEEL
Q09566;
                                                                                      Kirsten J.;
                                                                                                           STRAIN-Bristol N2;
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGYTGRYCQVRCSLQCVHGRFREEECSCVC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFRFNYGPTAQNVMIGHYTQVVWYRSYELGCAIAYCPDQPTYKYYQVCQYCPGGN--IRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWSNKTAQNAQRSANQCTLEHTSKEERTIDGVECGENL-FFSSAPYTWSYAIQNWFDERK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKYTPYSIGPPCGDCPDACD --
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242 AA;
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                                                                                                                                                                                 Peloderinae;
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                   40, Last annotation update)
kDa protein F48E8.1 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27493 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%; Score 226; DB 1;
25.6%; Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                 Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                            312
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TPX1_HUMAN
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Best Local
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ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; FALSE_NEG
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPX1_HUMAN STANDARD; PRT; 243 AA.
p16562;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Testis-specific protein TPX-1 precursor (Cysteine-rich secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D., Donner P., Schleuning W.-D.;
"The human cysteine-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
Eur. J. Biochem. 236:827-836(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; F48E8.1; CE01953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U23514; AAC46538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          similarity to a sperm-coa
Genomics 5:527-534(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.; "Cloning and mapping of a testis-specific gene with sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=90129048; PubMed=2613236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                         MEDLINE=96270732; PubMed=8665901;
                                                                                                                                                                                                                                                                                   TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-2) (Crisp-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 WPPQLQEQAPMAGALNRKE---SFL---LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVFVTARGQLYAMPAFTWASGDNGKCSNCPANAPACYQ-----GLCYMPKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIIPYKKG-----AW-----CSLCTASVSGCFKAWDHAGGLCEVPRN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHC----CGHYVQVVWAKTNLVGCGFSRCRDVQGVWGRGHRNVFVCHYNPQGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GECARNATCTHYTQLVWATSSQLGCGRHLCSA-----GQTAIEAFVCAYSPGGNWEVNGK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRHADTCDFRHSR-----GRINVGENIWAAP--YSNYSDAISIWFNEVHNPRCGCNHAY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQR----YSHAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPSHFQSD---SGLLSRSEHPNEYLKKWITHEHNRYRRMV--PASDMNMLYWSDELAASA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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299
312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sperm-coating glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 P
303 P
35054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%; Score 224; DB 1; 29.7%; Pred. No. 5.1e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEFC7BFF25E26288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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CRS1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                  CRS1_HUMAN STANDARD; PRT; 249 AA. P54107; Q13248; O00698; Q14082; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Cysteine-rich secretory protein-1 precursor (Ac glycoprotein homolog) (AEG-like protein) (ARP).
      Kraetzschmar J.,
                            SEQUENCE FROM N.A. MEDLINE-96270732; F
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                     AEGL1 OR CRISP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M25532; AAA61220.1; -. EMBL; X95239; CAA64526.1; -. PIR; B33329; B33329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testis; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001283; Allrgn_V5/Tpx1
Pfam: PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 187430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 DPTSWSSAIQSWYDEILDFVYGVGPKSPNAVVGHYTQLVWYSTYQVGCGIAYCPNQDSLK
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TISSUE SPECIFICITY: TESTIS AND EPIDIDYMIS.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGLCEVPRNPCRMSC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYYVCQYCPAGN-NMNRKN-TPYQQGTPCAGCPDDCDKGLCTNSCQYQDLLSNCDSLKNT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAFVCAYSPGGNWEVNGKTIIPYKKGAWCS------LCTAS-----VSGCFKAWDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCEHELLKEKCKATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAVSPPASNMLKMEWSREVTTNAQRWANKCTLQHSDPEDRKTS----TRCGENL-YMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQLLPA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVTVLLPSLPAEGKDPAFTALLTT-----QLQVQRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLAVLL------ALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:12024; TPX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
      Haendler B.,
                               . (LONG AND SHORT ISOFORMS),
PubMed=8665901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27259 MW; C5FE698C449CFAD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 221; DB 1;
Pred. No. 6.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TESTIS-SPECIFIC PROTEIN TPX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
Eberspaecher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 243;
u.,
                                                                                                                                                                                                                                                                                                        (Acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Indels
                                                            AND SEQUENCE OF 22-41.
Roostermann
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                                                                                                                                                                                                                                                                                                        epididymal
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                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                              CARBOHYD
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

Glycoprotein; Signal; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOm; PD000542; Allrgn_V5/Tpx1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X95237; CAA64524.1;
EMBL; X95238; CAA64525.1;
EMBL; S80310; AAB35899.1;
EMBL; D38451; BAA07483.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- FUNCTION: MAY HAVE A ROLE IN SPERM-EGG FUSION AND MATURATION.
-I- SUBCELLULAR LOCATION: LOCATED IN THE LUMEN AND EPITHELIUM OF DISTAL DUCTUS EFFERENTES AND EPIDIDYMAL DUCTS, AND ON THE POSTACROSOMAL REGION OF THE SPERM HEAD.
-I- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form/CRRSP-1 delta; may be produced by alternative splicing.
-I- TISSUE SPECIFICITY: CAPUT, CORPUS, AND CAUDA REGIONS OF THE EPIDIDYMIS, THE DUCTUS DEFERENS, SPERM, AND SEMINAL PALSMA.
-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCE/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi M., Fujimoto S., Takano H., Ushiki T., Abe K., Ishikura H., Yoshida M.C., Kirchhoff C., Ishibashi T., Kasahara M.; "Characterization of a human glycoprotein with a potential role in sperm-egg fusion: cDNA cloning, immunohistochemical localization, and chromosomal assignment of the gene (AECLI)."; Genomics 32:367-374(1996).
                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:304; AEGL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donner P., Schleuning W.-D.;
"The human cysteine-rich secretory protein (CRISP) family.
"Tructure and tissue distribution of CRISP-1, CRISP-2 and Eur. J. Biochem. 236:827-836(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the human acidic epididymal glycoprotein-like molecule: isolation of cDNA and tissue localization."; hokkaido Igaku Zasshi 70:743-753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96435914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96103955; PubMed-8543280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG ISOFORM).
                                          91
                                                                                                         31 PQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCG
M----TESNPLERRLPNTFCGENMHMTSYPV-SWSSVIGVWYSESTSFKH--GEWTTTDDD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601193;
                                    IPTPSLASGLWRTLQ----VGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECAR----N 144
                                                                            PNVQEE - - - - - - -
                                                                                                                                                                     Similarity
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                22
230
178
179
                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . (LONG ISOFORM), AND CHARACTERIZATION PubMed=8838800;
                                                                                                                                                                                                                                                                                21
249
230
178
249
                                                                       -----IVNIHNALRRRVVPPASNMLKMSWSEEAAQNARIFSKYCD 83
                                                                                                                                                                                                                         28481 MW;
                                                                                                                                                                                                                                              22
97
                                                                                                                                                                 8.4%; Score 213.5; DB 1
27.2%; Pred. No. 2.8e-10;
                                                                                                                                                   40;
                                                                                                                                                                                                                                    N-LINKED (GLCNAC...).
E -> D (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
K -> E (IN REF. 2 AND 3).
T -> A (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                    CYSTEINE-RICH SECRETORY PROTEIN-1.
                                                                                                                                                                                                                         85BED3DDEAD62A9C CRC64;
                                                                                                                                                  Mismatches
                                                                                                                                                                                    DB 1;
                                                                                                                                                   90;
                                                                                                                                                  Indels
                                                                                                                                                                                    Length
                                                                                                                                                                                    249;
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PERSULA REPORT OF SECOND SECON
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01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update)
Neurocan core protein precursor (245 kDa early postnatal core
glycoprotein) [Contains: 150 kDa adult core glycoprotein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulated, aggs
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92406907; PubMed-1326557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                  use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.; "Cloning and primary structure of neurocan, a developmentally regulated, aggregating chondroitin sulfate proteoglycan of brain."; J. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSPG3 OR NCAN
  EMBL; M97161; HSSP; P00740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94230574; PubMed-7513709; Friedlander D.R., Milev P., Karthikeyan L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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                                                                                  tities requires a license agreement (See http://www.isb-sib.ch/announce/
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     IN KIDNEY, LUNG, LIVER AND MUSCLE.

PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).

PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DECRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGN-WEVNGKTIIPYKKGAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-CAM). CHONDROITIN SULFATE PROTEOGLYCAN;
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Best Local
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PROSITE; PS00010; ASX_HVDROXYL; 1.

PROSITE; PS00022; EGF_1; 3.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-Like domain; Calcium; Repeat; Lectin; Sushi: Simal
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pF00193; xlink; 2.
om; pD000918; Link; 2.
T; SM00032; CCP; 1.
T; SM00034; CLECT; 1.
T; SM0019; EGF_CA; 1.
T; SM00101; EGF_like; 1.
T; SM00409; IG; 1.
NPCLHGGTCRTNGTMYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVNGFICLCL 1014
                                                                                              AFVCAYSPGGNWEVNGKTIIPYKKGAWCS--LCTASVSGCFKAWDHAGGLCEVPRNPCRM
                             SCQNHG----RLNISTCHCHCPPGYTGRYCQV-----RCSLQCVHGRFREEECS----CVCD
                                                                ASVSSGEPTRLWDI-PSTLIPVSLGLDESDLKVVAESPGLEGFWEEVASGQEDPTDPCEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00059; lectin_c; 1.
                                                                                                                                . Similarity 24.8 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000436;
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Ig_MHC.
Lectin_C.
                                                                                                                                              8.4%;
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EGF-like.
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                                                                                                                                 34;
                                                                                                                            Score 212; DB
Pred. No. 2e-0
34; Mismatches
                                                                                                                                                                                                    M.
                                                                                                                                                                                                               BY SIMILARITY
N-LINKED (GLCNU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSHI
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EGF-LIKE 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROCAN CORE PROTEIN.
150 KDA ADULT CORE GLYCOPROTEIN
IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN
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                                                                                                                                                                 DB 1;
                                                                                                                                 134;
                                                                                                                                                               Length 1257;
                                                                                                                                                                                                                  .) (POTENTIAL).
                                                                                                                                                                                                                                                .) (POTENTIAL).
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(CHONDROITIN SULFATE).
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                                                                                           or send
PIR; A49202; A49202.
MGD; MGI:102553; Aeg1.
InterPro; IPR001283; A
Pfam; PF00188; SCP; 1.
                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sperm-coating glycoprotein 1 precursor (SCP 1) (Acidic glycoprotein 1) (Cysteine-rich secretory protein-1) (Crabell Or AEG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse submandibular glands express an androgen-regulated encoding an acidic epididymal glycoprotein-like molecule." Mol. Cell. Endocrinol. 89:25-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Submandibular gland; MEDLINE~93307144; PubMed=8319566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizuki N., Kasahara M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93246016; PubMed=1301383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Submandibular gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                     INDUCTION: By androgens.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE
                                                                                                                                                                                                                                                                                                            CONVOLUTED TUBULES CELLS.

TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDYMIS WHERE IT IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN. BINDS TO THE HEADS OF SPERMATOZOA. ALSO EXPRESSED IN THE
                                                                                                                                                                                                                                                                        AFTER BIRTH.
                                                                                                                                                                                                                                                                                                 SUBMANDIBULAR GLAND
                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
                                                       M92849; AAA37185.1;
L05559; AAA37460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNF-----FAGGEDCVVMVAHENGRWNDVPCNYNLPYVCK 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEHKFI--------NSFGHENSWIGLNDRTVERDFQWTDNTGLQYENWREKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSYGGNLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
          Allrgn_V5/Tpx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                               Usage
                                                                                                                                                                                                                                                                                 BETWEEN DAYS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442
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Best Local
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ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP, 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Sperm; Glycoprotein; Signal.
SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                      PGCV_RAT STANDARD; PRT; 2/30 An.
Q9ERB4; 008592; 088564; Q9R1K4;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                           Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding proteoglycans in developing brain: aggrecan, versican, neuro
                                                                                                                                                                                                                               (ISOFORM V3), AND SEQUENCE STRAIN-Wistar Kyoto;
MEDLINE=99327053; PubMed=1
                                                                                                                                                                                                                                                         [1]
SEQUENCE OF 349-2738 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _RAT
                                      Biochem.
                                                                                                                     STRAIN=Wistar Kyoto;
MEDLINE=98308094; Pu
TISSUE=Kidney;
            SEQUENCE OF 2421-2463
                                                     brevican.
                                                                                                     Milev P., Maurel P., Chiba A., Mevissen M., Popp
                                                                                                                                              SEQUENCE OF 349-2738 FROM N.A. (ISOFORM VO).
                                                                                                                                                                      "Versican/PG-M isoforms in vascular smooth muscle cel
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                       Wight
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                  Lemire J.M., Braun
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFL-----LLSLHNRLRSWVQPPA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GHEDKYTNCKYLKKMLSCEH-ELLKKGCKATC-----LCEGKIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISTCHCHCPPGYTGRY--CQ-VRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGNYQ--GRLYTPYTAGEPCASCP-----DHCEDGLC---TNSC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGWYNEYKDLTYDVGPKQPDSVVGHYTQVVWNSTFQVACGVAECPKNPLRY-YYVCHYCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHA-GGLCEVPRNPCRMSCQNHGRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDLLKMEWNYDAQVNAQQWADKC---TFSHSPIELRTTNLRCGENL-FMSSYLASWSSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRT--LQVGWNMQLLPAGLASFVEVV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMLVLFFL----AAVLPPSLLQDSSQENRLEKLSTTKMSVQEEIVSKHNQLRRMVSPSG
                                                                                                                                                                                                       T.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                      Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                 PubMed=10397680;
n K.R., Maurel P.,
                                                                                                                     PubMed=9642104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%;
25.7%;
            FROM N.A.
                                      Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 209; Db .,
No. 6.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM-COATING GLYCOPROTEIN 1
N-LINKED (GLCNAC. . .) (POTE); D00DD0348F85781F CRC64;
                                                                                                                                                                                                                                                          1. (ISOFORM 2657-2738
                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                      247:207-212(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 110;
            (ISOFORM VO)
                                                                                                                                                                                                                 Kaplan
                                                                                                                                                                                                                                                          VO),
                                                                                                                                                                                                               E.D.,
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 244;
                                                                                                     s;
                                                                                                                                                                                                                 Schwartz S.
                                                                                                                                                                                                                                                         (ISOFORM
                                                                                                                                                                                       cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                       Yamaguchi
                                                               neurocan,
                                                                                                                                                                                                                                                         VINT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244
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                                                               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
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SMART; SM00032; CCF; 1.

SMART; SM00034; CLECT; 1.

SMART; SM000181; EGF; 2.

SMART; SM001019; EGF_CA; 2.

SMART; SM00409; IG; 1.

SMART; SM004409; IG; 1.

SMART; SM004409; IG; 1.

SMART; SM004410; IG_11ke; 1.

SMART; SM004410; ASX_HYDROXYL; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1; 1.

PROSITE; PS000615; EGF_1; 2.

PROSITE; PS00022; EGF_1; 2.

PROSITE; PS01180; EGF_CA; 1.

PROSITE; PS01180; EGF_CA; 1.

PROSITE; PS011241; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR0007481; EGF_Ca.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003504; Ig_like.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000438; Link.
InterPro; IPR000438; Sushi_SCR_CCP.
InterPro; IPR000438; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE=Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
"Molecular cloning and characterization of two developme regulated genes in rat lung.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., "Proteoglycan expression in the normal rat kidney."; Nephron 77:461-470(1997).
                               Hyaluronic
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
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                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                      Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 2535-2738 FROM N.A.
NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PRODUCTS: At least 3 isoforms; VO (Shown here), Vint; are produced by alternative splicing. TISSUE SPECIFICITY: In kidney is expressed in the papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: May play a role in intercellular signaling and connecting cells with the extracellular matrix. May take
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        but not in glomeruli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY007691;
P01132; 1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF084544; AAD48544.1; -. AF072892; AAC26116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF062402; AAC40166.1; -.
                                                                                                                                                                                                                                                                                                                                                               PR01265; LINKMODULE
                                                      acid; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB51125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG16631.1;
                                                                                                                                                                                                                                                                                                                                                                               _SCR_CCP.
                                   e splicing. POTENTIAL.
                    VERSICAN CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmentally
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                                                                                                                                                    LCEVPRNPCRMSCQNHGRLNISTCH-----CHCPPGYTGRYCQV-----
                                 FRWTDGSALQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTC
                                                 FRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYIC
                                                                  AAERECRLQGAHLTSILSHEEQ ---
                                                                           RARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDS
                                                                                                   TCVDGLNTFR----
                                                                                                                  QCVHG--RFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYY
2632
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57
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1257
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1684
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1240
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2240
22711
27211
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                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                   2539
                                                                                                   -CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWD
                                                                                                                                                                            27.0%;
                                                                                                                                                                                                     300004
                                                                                                                                                                                  7.98;
                                                                                                                                                                    28;
                                                                                                                                                                                                    WW;
                                                                                                                                                                                                                                                                                                                                                                             G-TYPE LECTIN
SUSHI
BY SIMILARITY
                                                                                                                                                                  Score 200; DB 1, Pred. No. 4.1e-08; Standarches 84;
                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINK 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAG-ALPHA
                                                                                                                                                                                                             R -> RKWSFRKNGQPCFNKY (IN ISOFORM VINT).
AEREC -> NSARG (IN REF. 4).
                                                                                                                                                                                                                            MISSING (IN ISOFORM V3).
PSAYQRTYSKKYLKNSSSVKDNSINTSKHEHRWSRRWQETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                              N-LINKED
                                                                   -MFVNRV
                                                                                                                                                                                                      12CA626D58BD8C6A
                                                                                                                                                                                                                                    (IN ISOFORM V3)
                                                                                                                                                                                                                                                            (GLCNAC...
                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                             (GLCNAC.
                                                                                                                                                                                                                                                    (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCIUM-BINDING
                                                                                                                                                                                   Length 2738;
                                                                                                                                                                     Indels
                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                              (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                   WIGLNDKMFEHD
                                                                                                                                                                     64;
                                                                                                                                                     RCSL
                                                                                                                                                                     Gaps
                                                   441
                                                                    2578
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13;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "Functional annotation of Nature 409:685-690(2001).
           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6;
MEDLINE-95181355; PubMed-7876137;
MEDLINE-95181355; PubMed-7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q62059; Q62058; Q9CUUO;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibrobla:
(Chondroitin sulfate proteoglycan core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21085660; PubMed=11217851; Kawai J., Shinagawa A. Shihata v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).
STRAIN=C57BL/6J; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteoglycan generated by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain; MEDLINE=95122551; PubMed=7822336; Ito K., Shinomura T., Zako M., Ujita M., Kimata K.; "Multiple forms of mouse PG-M, a large chondroitin sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STRAIN-C57BL/6, and Swiss Webster; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSPG2
                                     V2 and V3; are produced by alternative splicing.
TISSUE SPECIFICITY: V2 is found only in brain.
DEVELOPMENTAL STAGE: Disappears after the cartilage development.
SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 EGTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                               hyaluronic acid.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 4 isoforms; V0 (shown here), V1,
                                                                                                                                                                                                                                                                                                                 FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
           SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem. 270:3914-3918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                             annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270:958-965(1995).
    entry is
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protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĀΑ
produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Mus
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SMART; SM00179; I
SMART; SM00001; I
SMART; SM00409; SMART; SM00445; I
               DISULFID DISULFID
                                                                   DISULFID
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DISULFID
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DOMAIN
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DOMAIN
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                       SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM000179; EGF_CA; 1.
SMART; SM00001; EGF_Like; 1.
SMART; SM00409; IG; 1.
                               DISULFID
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                                                                                                                                                                                                             Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin c
                                                                                                                        DOMAIN
                                                                                                                                                                                               Hyaluronic acid; Alternative splicing SIGNAL 1 20 POTENTIA:
                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                             ProDom; PD000918; Link; 2
                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0010;
                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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PF00193;
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PF00059; lectin_c; 1.
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E; PS00010; ASX_HYDROXYL; 1.

E; PS00022; EGE_1; 2.

E; PS01186; EGE_2; 1.

E; PS01187; EGE_CA; 1.

E; PS01241; LINK; 2.

E; PS01241; LINK; 2.

E; PS0041; C_TYPE_LECTIN_1; 1.

E; PS0041; C_TYPE_LECTIN_2; 1.
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| IPRO00742;
| IPRO01438;
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| IPRO03599;
| IPRO03004;
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| IPRO00538;
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Xlink;
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Lectin_C.
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P13611: P20754; Q9UNW5; Q13010; Q13189; Q15123;
O1-JAN-1990 (Rel. 13, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast (Chondroitin sulfate proteoglycan core protein 2)
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Mammalia; Eutheria;
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       SEQUENCE FROM N.A. (ISOFURE SECTION OF A STATE OF THE SECTION OF T
                                                                                                                                        Homo
                                                                                   NCBI_TaxID=9606;
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Characterization of the complete genomic structure
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                                                                                                                                       sapiens (Human).
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I -> T (IN REF. 3).
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                  Iozzo R.V.;
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versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                  MEDLINE-96213482; PubMed-8627343;
Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
"Differential expression of versican isoforms in brain tumors.";
J. Neuropathol. Exp. Neurol. 55:528-533(1996).
-i- FUNCTION: May play a role in intercellular circulina and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dours-Zimmermann M.T., Zimmermann D.R.;
"A novel glycosaminoglycan attachment domain identified alternative splice variants of human versican.";
J. Biol. Chem. 269:32992-32998(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zimmermann D.R., Ruoslahti E.; "Multiple domains of the large fibroblast proteoglycan, versican."; EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95181355; PubMed=7876137; Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; Without a chondroitin sulfate attachment in region in mouse and tissues.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 251-347 FROM N.A. MEDLINE=93122792; PubMed=1478664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krusius T., Gehlsen K.R., Ruoslahti E.;
"A. fibroblast chondroitin sulfate proteoglycan core protein contains
lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
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                                                                                                                                                                                                                                                        hyaluronate-binding protein.";
J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                    Perides G., Lane W.S., Andrews D., Dahl Isolation and partial characterization
                                                                                                                                                                                                                                                                                                                                                                                          "Versican/PG-M isoforms in vascular smooth muscle cells."; Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                          Wight
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Aortic smooth muscle; MEDLINE=99327053; PubMed=10397680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mapping of the versican proteoglycan human chromosome 5 (5q12-5q14).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McPherson
                                                                                                                                                                                                                                                                                                                       MEDLINE-89174663; PubMed-2466833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iozzo R.V., Naso M.F.,
                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissues.
FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part the regulation of cell motility, growth and differentiation. hyaluronic acid.

SUBCELLULAR LOCATION: Secreted; extracellular matrix. SUBCELLULAR LOCATION: At least 5 isoforms; V0 (shown here), V 2, V3 and Vint; are produced by alternative splicing. TISSUE SPECIFICITY: Cerebral white matter: V0 and V1 is expression normal brain, gliomas, medulloblastomas, schwannomas,
                                                                                                                                                                                                                                                                                                                                                                                                                          T.N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cannizzaro L.A., Wasmuth J.J.,
                                                                                                                                                                                                                                                                                         Dahl D., Bignami A.; ation of a glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene (CSPG2) to
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THE TENT OF THE TE
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SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00019; EGF_CA; 1.
SMART; SM00179; EGF_Like; 1.
SMART; SM00409; IG; 1.
SMART; SM00405; LINK; 2.
SMART; SM00445; LINK; 2.
                                                                                                                                                                                                              PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00102; EGF_1; 2.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01241; LINK; 2.

PROSITE; PS01241; C_TYPE_LECTIN_1; 1.

PROSITE; PS00415; C_TYPE_LECTIN_2; 1.

Clycoprotein; Proteoglycan; Lectin; Extracellular matrix; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin d
                                                                                             DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                      SIGNAL
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF-2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:2464; CSPG2.
MIM; 118661; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; S06014; S06014.
; A29348; A29348.
; A30358; A30358.
P; P01132; 1EGF.
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOWAIN.

SIMILARITY: CONTAINS 2 LINK DOWAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOWAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOWAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOWAIN.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; PF00008; EGF; 2.
n; PF00047; 19; 1.
n; PF00059; lectin_c; 1.
n; PF00084; sushi; 1.
n; PF00193; X1ink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurofibromas, and menningiomas; v2 is restricted to and gliomas; v3 is found in all these tissues except medulloblastomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000436;
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IPR001304;
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                                                                                                                                                                                             acid;
                                                                                                                                                                                             Alternative
                                             3396
137
244
346
1335
3089
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Ig_MHC.
Lectin_C.
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EGF_Ca.
EGF_II.
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                                                                                                                                                                                                            domain; Calcium; Immunoglobulin
                                                                 LINK 1
LINK 2
                                                                                                                                                                                             splicing
                    DOMAIN)
                                     GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                 VERSICAN CORE I
                                                                                                                                                                    POTENTIAL.
                                                                                                               PROTEIN.
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Best Local
                                              __MOUSE
__MOUSE STANDARD; PRT; 243 AA.
P16563;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1996 (Rel. 15, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Testis-specific protein TPX-1 precursor.
TPX1 OR TPX-1
                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                          Mus musculus (Mouse).
                                                                                                                                                     3243
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                                                                                                                                                                                                                                                          3096 NPC-----LNGGTCYPTETSYVCTCVPGYSGDQCELDFDECHSNPCRNGATCVDGF 3146
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DISULFID
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                                                                                                                                                                                                                                             272
                                                                                                                                                                                                                                                                          230 NPCRMSCQNHGRLNISTCH------CHCPPGYTGRYCQV------RCSLQCVHG- 271
                                                                                                                                                 STLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 3290
                                                                                                                                                                                                QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG
                                                                                                                                                                   EHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                       NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC
                                                                                                                                                                                                                                         -RFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKC
                                                                                                                                                                                      RLQGAHLTSILSHEEQ----MFVNRV-----GHDYQ---
                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                   330
615
782
809
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1398
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11863
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2272
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615
782
809
1338
1398
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14663
14663
2179
2277
2280
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3162
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33352
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                      Score 196; DB 1;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
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N-LINKED
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EGF-LIKE 2, CA
C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
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                                                                                                                                                                                      -WIGLNDKMFEHDFRWTDG
                                                                                                                                                                                                                                                                                                              Length 3396;
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(POTENTIAL).
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(POTENTIAL).
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Murinae; Mus

SEQUENCE FROM N.A NCBI_TaxID=10090; [1]

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В
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Search completed: December 29, Job time : 44 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Testis;

MEDLINE-90129048; PubMed-2613236;

Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;

"Cloning and mapping of a testis-specific gene with sequence similarity to a sperm-coating glycoprotein gene.";

Genomics 5:527-534(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04284; 1CFE.
MGD; MGI:98815; Tpx1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: TESTIS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                        196
                                                                                                                                                                                                                                                                   154 VWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSG 213
                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                141 VWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKST--PYQQGTPCASCPNN---
                                                                                                                                                                                                                                                                                                                  101 MSTDPTLWST-----
                                                                          228 LKTKCQATC-----LCEDKIH 243
                                                                                                                                                                                        214 CFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRF 273
                                                                                                                                                                                                                                                                                                                                                                                  11 IVNKHNELRRSVNPTGSDILKMEWSIQATTNAQKWANKCILEHSSKDDRKINIRCGENLY 100
                                                                                                                                                                                                                                                                                                                                                                                                                           51 LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPS-----LASG---- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                               REEECSCVCDIGYGGAQCATKVH 296
                                                                                                                                                                                                                                                                                                                                                  -----LWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 22 POTENTIAL.
23 243 TESTIS-SPECIFIC PROTEIN TPX-1.
243 AA; 27605 MW; 6E707F569ACAA244 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                     ·CE--NGLCTNSCDFEDLL--SNCE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 193.5; DB 1; Length 243; 24.0%; Pred. No. 1.1e-08; Indels 77
                                                                                                                                                                                                                                                                                                           -----VIQSWYNENEDFVYGVG-AKPNSAVGHYTQL 140
                  2002, 02:23:56
                                                                                                                                                     ----SLKTSAGCKH-EL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 77;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                               250
236
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                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                       PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-944-896-50
2529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                               283224 segs, 96134422 residues
MLHPETSPGRGHLLAVLLAL......RNRYICQFAQEHISRWGPGS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                       pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                                              Length
DB
                                      JE0204
A55535
A60979
A33329
A47171
T14274
T42389
A248925
T22436
A24609
F44583
J01693
T201693
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T201693
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$68684
$28764
A49202
               VCTO14
T08126
S26238
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                                                                      versican precursor
versican precursor
mannose receptor p
hypothetical prote
acidic epididymal
venom allergen ant
                                                                                                                    hypothetical prote cysteine-rich secr cysteine-rich secr neurocan precursor cysteine-rich secr testicular protein versican precursor versican precursor testis-specific prohondroitin sulfat
     pathogenesis-relat
hypothetical prote
pathogenesis-relat
venom allergen ant
pathogenesis-relat
pathogenesis-relat
pathogenesis-relat
pathogenesis-relat
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testis-specific, v
                                                                                                                                                                                                                      neutrophil granule neurocan - mouse
                                                                                                                                                                                                                                              Description
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45 173	44 173	43 173.5	42 173.5					37 175							
6.8	6.8	6.9	6.9	6.9	6.9	•	•	6.9	-	-		•	-	•	-
883	209	213	212	204	168	208	205	168	185	161	178	2825	202	1456	184
Ν	N	N	N	Ŋ	N	N	N	N	N	N	N	N	N	Н	N
S49126	T19848	T22439	T27834	A44583	C24620	T19852	T48294	T07146	T10677	S65777	S68681	T14271	G44583	A36563	S10205
brevican precursor	hypothetical prote	hypothetical prote	hypothetical prote	venom allergen ant	pathogenesis-relat	hypothetical prote	pathogenesis relat	pathogenesis-relat	. pathogenesis-relat	pathogenesis-relat	cysteine-rich secr	Doc4 protein, stre	venom allergen ant	mannose receptor p	pathogenesis-relat

ALIGNMENTS

r det	# # # # # # # # # # # # # # # # # # #			[le si					
QY 184 PGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLN 243	KEAAANAQKWANQCNYRHSNPKDRWTSLKCC QRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHI :	Qy 13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAA 67	Query Match 9.9%; Score 250; DB 2; Length 245; Best Local Similarity 27.1%; Pred. No. 9.5e-12; Matches 76; Conservative 44; Mismatches 108; Indels 52; Gaps 12;	C;Genetics: A;Gene: SGP28 C;Superfamily: cysteine-rich secretory protein 1 C;Superfamily: cysteine-rich secretory protein 1 F;1-19/Domain: signal sequence #status predicted <sig> F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <ma< th=""><th>A;Accession: \$68683 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-105,'S',107-245 <kra> A;Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819</kra></th><th>A; Riderizschindi, J.; Addititi, B.; Enderspacetiet, D.; ROOS CEINGI, D.; Donnet, F., Schie Bur. J. Blochem. 236, 827-836, 1996 A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure A;Reference number: S68681; MUID:96270732; PMID:8665901</th><th>PIDN:CAA63984.1; PID:g1213613</th><th>ranules</th><th>phil granules matrix glycoprotein SGP28 precursor ies: Homo sapiens (man): 15-Feb-1997 #sequence_revision 13-Mar-1997 #textssion: S68691; S74313; S68683 dsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaardett. 380, 246-250, 1996</th><th>RESULT 1 S68691</th></ma<></sig>	A;Accession: \$68683 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-105,'S',107-245 <kra> A;Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819</kra>	A; Riderizschindi, J.; Addititi, B.; Enderspacetiet, D.; ROOS CEINGI, D.; Donnet, F., Schie Bur. J. Blochem. 236, 827-836, 1996 A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure A;Reference number: S68681; MUID:96270732; PMID:8665901	PIDN:CAA63984.1; PID:g1213613	ranules	phil granules matrix glycoprotein SGP28 precursor ies: Homo sapiens (man): 15-Feb-1997 #sequence_revision 13-Mar-1997 #textssion: S68691; S74313; S68683 dsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaardett. 380, 246-250, 1996	RESULT 1 S68691

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A;Cross-references: GDB:683195
C;Superfamily: yellowjacket venom allergen antigen
C;Keywords: brain
                                                                                                                                                                                                                                               R; Murphy, E.V.; Zhang, Y.; Zhu, W.; Biggs, J. Gene 159, 131-135, 1995
A;Title: The human glioma pathogenesis-related A; Reference number: JC4131; MUID:95331646; PMIC A; Accession: JC4131
                                                                                                                                                                                                                                                                                                                                                        JC4131
glioma pathogenesis-related protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 04-Mar-2000
C;Accession: JC4131
C;Accession: JC4131
                                                                                                                                A; Experimental source: brain tumor C; Genetics:
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A;Residues: 1-1268 <ARU>
A;Residues: 1-1268 <ARU>
A;Cross-references: EMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g758630
A;Cross-references: EMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g758630
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;
f;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: EGF homology <EGF>
F;964-995/Domain: EGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
                                                                                                            A; Gene: GDB: GLIPR
                                                                                                                                                                            A;Cross-references: GB:U16307; NID:g1100927; PIDN:AAA82731.1;
                                                                                                                                                                                                        A; Molecule type:
A; Residues: 1-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
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A;Description: Amino acid sequence of mouse neurocan and brevican and A;Reference number: S52781
A;Accession: S52781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1167-1223/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurocan - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC----TASVSGCFKAWDHAGGLCEVPRNP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CENNPCLHGGTCHTNGTVYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVN 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWREKQPDNF-----FAGGEDCVVMVAHESGRWNDVPCNYNLPYVCK 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFICLCLPSYGGSLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGH 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRMSCQNHGRLNISTCH-----CHCPPGYTGRYCQV-----RCSLQCVHGRFREEECS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASVSSGEPTGLWDI-PSTLIPVSLGLDESVLNVVAESPSVEG---FWEEVASGQEDPTDP 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSVHSPEEHKFI------NSFGHENSWIGLNDRTVERDFQWTDNTGLQYE 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVC 282
                                                                                                                                                                                                      1-219 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S52781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 119; Indels
                                                                                                                                                                                                                                                                              ated protein is PMID:7607567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                     structurally related
                                                                                                                                                                            PID:g847722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
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                                                                                                            R:Kirsten, J.
submitted to the EMBL Data Library, March
A; Molecule type: DNA A; Residues: 1-312 <K
                                         A;Reference number: S59413
A;Accession: T16415
A;Status: preliminary; translated from GB/EMBL/DDBJ
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RESULT 5
T16415
hypothetical protein F48E8.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 97-100;114-120;134-144 <RIC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 01-May-1997 #sequence_revision 01-May-1997 #text_change 19-May-2000
C;Accession: JC5308; PC4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: yellowjacket venom allergen antigen 5
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-266/Product: testis-specific, vespid, and pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: brain tumor C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 180, 125-130, 1996
A;Title: RTVP-1, a novel human gene with sequence similarity
A;Reference number: JC5308; MUID:97128816; PMID:8973356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;233-255/Domain: transmembrane #status predicted <TMM>
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A; Residues: 1-266 < RIC1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: rtvp-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: PC4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X91911; NID:g1030052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC5308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           testis-specific, vespid, and pathogenesis-related protein 1 precursor - human
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Best Local
                                                                                                                                                                                                                                                              154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC
                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                              31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 ESFL---LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.; Chen, P.;
                                                                                                                                                                                                             VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT----WPYKRGATCSAC
                                                                                                                                                                                                                                                                                                                 PNFTS-----LGENIWTGSVPIFSVSSAITNWYDEIQDYDFKTRICKK-~VCGHYTQV
                                                                                                                                                                                                                                                                                                                                                                                                                      EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH
                                                                                                                                                                                                                                                                                                                                                                     PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Furman, F.; Huynh, N.; Israel, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%; Score 231; 32.4%; Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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Pred. No. 2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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cosmid F48E8

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A;Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883 R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donne Eur. J. Biochem. 236, 827-836, 1996 A;Title: The human cysteine-rich secretory protein (CRISP) family. Primar A;Reference number: S68681; MUID:96270732; PMID:8665901 A;Accession: S68682
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                                                                                                                                                                                                                                                                                                                A;Map position: 6p21-6qter
C;Superfamily: cysteine-rich secretory protein 1
F;1-20/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning and mapping of a testis-specific gene with sequence similarity A;Reference number: A33329; MUID:90129048; PMID:2613236 A;Accession: B33329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, Genomics 5, 527-534, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000
C;Accession: B33329; S68682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine-rich secretory protein 2 type I precursor - N;Alternate names: testis-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 28/1;
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A;Map position: 6p21-6qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-243 < KRA>
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:TPX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-243 <KAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X95239; NID:g1262816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                            21-243/Product: cysteine-rich secretory protein 2 type I *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 WPPQLQEQAPMAGALNRKE---SFL---LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                             49
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ns: 28/1; 94/3; 153/3; 174/3; 226/3
                                                                                                                                                                  13 LLAVLL------ALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLR 59
                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GECARNATCTHYTQLVWATSSQLGCGRHLCSA-----GQTAIEAFVCAYSPGGNWEVNGK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQR----YSHAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIIPYKKG-----AW-----CSLCTASVSGCFKAWDHAGGLCEVPRN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHC----CGHYVQVVWAKTNLVGCGFSRCRDVQGVWGRGHRNVFVCHYNPQGN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPSHFQSD---SGLLSRSEHPNEYLKKWITHEHNRYRRMV--PASDMNMLYWSDELAASA 113
  GLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAI 175
                                           KAVSPPASNMLKMEWSREVTTNAQRWANKCTLQHSDPEDRKTS----TRCGENL-YMSS 102
                                                                                  SWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQLLPA 115
                                                                                                                           LVTVLLPSLPAEGKDPAFTALLTT-----QLQVQRE---
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Pred. No. 1.1e-09;
                                                                                                                                                                                                                               Score 221; DB 2; Pred. No. 1.5e-09;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                    predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA64526.1; PID:g1262817
                                                                                                                                                                                                                                                 Length 243,
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A; Residues: 1-249 < KRA>
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27.2%;
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A:Molecule type: mRNA
A;Residues: 1-1257 <RAU>
A;Residues: 1-1257 <RAU>
A;Cross-references: EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650
A;Cross-references: EMBL:M97161; NID:g205649; complement factor H repeat homology;
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
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A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure A;Reference number: 588681; MUID:96270732; PMID:8665901
A;Accession: 588684
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C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                neurocan precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Accession: S28764
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                                                                                                                                                                                                                                          J. Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggr A;Reference number: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCG 90
                                                                                                                                                                                                                                                                                                                                                   U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K. Chem. 267, 19536-19547, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M -- TESNPLERRLPNTFCGENMHMTSYPV -SWSSVIGVWYSESTSFKH -- GEWTTTDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
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В
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Endocrinology 133, 192-198, 1993
A;Title: Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG) and the nov A;Reference number: A49202; MUID:93307144; PMID:8319566
A;Accession: A49202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;23-1257/Product: neurocan #status predicted <MAT>
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-c) motif
F;953-984/Domain: EGF homology <EGF>
F;1029-1119/Domain: C-type lectin homology <LCH>
F;1029-1119/Domain: complement factor H repeat homology <FHD>
F;1121/Domain: complement factor H repeat homology <FHD>
F;121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C:Accession: A49202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: nucleic acid
A; Residues: 1-244 <HAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine-rich secretory protein-1 - mouse N; Alternate names: CRISP-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A49202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
         185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1015 PSYGGNLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSP 1070
                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 897 ASVSSGEPTRIMDI-PSTLIPVSLGLDESDLKVVAESPGLEGFWEEVASGQEDPTDPCEN 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AFVCAYSPGGNWEVNGKTIIPYKKGAWCS--LCTASVSGCFKAWDHAGGLCEVPRNPCRM 234
                                                                                                                                                                                58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                   w
GGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHA-GGLCEVPRNPCRMSCQNHGRLN 243
                                                      QGWYNEYKDLTYDVGPKQPDSVVGHYTQVVWNSTFQVACGVAECPKNPLRY-YYVCHYCP 172
                                                                                                             SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSP 184
                                                                                                                                                                          SDLLKMEWNYDAQVNAQQWADKC---TFSHSPIELRTTNLRCGENL-FMSSYLASWSSAI 113
                                                                                                                                                                                                                                ADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRT--LQVGWNMQLLPAGLASFVEVV 124
                                                                                                                                                                                                                                                                                                                                                 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFL-----LLSLHNRLRSWVQPPA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNF-----FAGGEDCVVMVAHENGRWNDVPCNYNLPYVCK 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                                                                                          LMLVLFFL----AAVLPPSLLQDSSQENRLEKLSTTKMSVQEEIVSKHNQLRRMVSPSG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPCLHGGTCRTNGTMYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVNGFICLCL 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                    . Similarity 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 8.4%; Score 212; DB 2; Similarity 24.8%; Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 209; DB 2;
25.7%; Pred. No. 1.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 244;
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2397 <RES>
A;Residues: 1-2397 <RES>
A;Cross-references: GB:DI6263; NID:g862460; PIDN:BAA03796.1; PID:g862461
A;Cross-references: GB:DI6263; NID:g862460; Complement factor H repeat homology; Csuperfamily: versican; C-type lectin homology; complement factor H repeat homology; F;1-20,Domain: signal sequence #status predicted <SIG>
F;21-1654/Domain: versican #status predicted <MAT>
                                                                                                                                                                                                                   R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K. J. Biol. Chem. 270, 958-965, 1995
A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate A;Reference number: A55535; MUID:95122551; PMID:7822336
A;Accession: A55535
                                                                                                                                                                                                                                                                                                                                                            N;Contains: glial hyaluronate-binding protein C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: A55535
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                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     versican
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: chondroitin sulfate proteoglycan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-243 <MAE>
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C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 HCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVCDIGYGGAQCATKVH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 NYMKKST--PYHQGTPCASCP---NNC----DNGLC---TNSCDFEDL-----LSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 WEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 YEENENFVFGVG-AKPNSAVGHYTQLVWYSSFKVGCGVAYCPNQDTLKYFYVCHYCPMGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ISTCHCHCPPGYTGRY--CQ-VRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VFAVLLPLPPTEGKDPDFATLTTNQIQVQRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LLAVLLALLGT-----TWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NILKMEWNVQAAANAQKWANNC-ILEHSSTEDRKINIKCGENL-YMSTDPTSWRTVIQSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLW 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 8.2%; Score 208; DB 2;
Similarity 25.5%; Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SLKSSAGCKHELLKAKCEATCLCE------DKIH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHEDKYTNCKYLKKMLSCEH-ELLKKGCKATC-----LCEGKIH
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A. Molecule type: protein
A. Molecule type: protein
A. Rolecule type: protein
A. Residues: 24-50;80-87,'D',89-119;128-155;167-218;229-259,'IR';261-268;277-283,'G',285-4, R: Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 262, 13120-13125, 1987
A. Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A. Reference number: A29348; MUID:88007514; pMID:2820964
                                                                                                                                                                                                                        R:Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2468833
A;Accession: A30358
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 208-440;1094-1385;1910-2246 < YAO>
A; Residues: 208-440;1094-1385;1910-2246 < YAO>
R; Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A; Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A; Reference number: A60979; MOID:89229983; PMID:2469524
A; Accession: A60979
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A;Residues: 1-2409 <ZIM>
A;Cross-references: GB:X15998; NID:g37662; PIDN:CAA34128.1; PID:g37663
R;Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001 C;Accession: S06014; S43921; A60979; A30358; A29348; A45131; T54179 R;Zimmermann, D.R.; Ruoslahti, E.
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 171-210; 289-303 <BIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells A;Reference number: S43921; MUID:95005762; PMID:7921538 A;Accession: S43921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Multiple domains of the large fibroblast proteoglycan, versican. A; Reference number: S06014; MUID:90059882; PMID:2583089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Zimmermann, D.R.; Ruoslal
EMBO J. 8, 2975-2981, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      versican precursor - human
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
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F:265-246/Domain: link protein repeat homology <LNK2>
F:2095-2126/Domain: BGF homology <EGI>
F:2133-2164/Domain: EGF homology <EG2>
F:2171-2291/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2194 AAERECRLQGAHLTSILSHEEQ----MFVNRV-----GHDYQ----WIGLNDKMFEHD 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2094 LCKT--NPC------LNGGTCYPTETSYVCTCAPGYSGDQCELDFDECHSNPCRNGA 2142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POCAT
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C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; F;1-20/Domain: signal sequence #status predicted <SIG>F;21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>F;167-244/Domain: link protein repeat homology <LINK1>F;165-346/Domain: link protein repeat homology <LINK2>F;265-346/Domain: link protein sulfate attachment #status predicted <GAG>F;2106-2137/Domain: EGF homology <EG1>F;2106-2137/Domain: EGF homology <EG2>F;2144-2175/Domain: EGF homology <EG2>F;2144-2175/Domain: EGF homology <EG2>F;2144-2175/Domain: C-type lectin homology <LCH>F;216-2302/Domain: C-type lectin homology <LCH-F;216-2302/Domain: C-type lectin homology <
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <KAS>
                                                                                                                                        Genomics 5, 527-534, 1989

A;Title: Cloning and mapping of a testis-specific gene with sequence similarity to a A;Reference number: A33329; MUID:90129048; PMID:2613236

A;Accession: A33329
                                                                                                                                                                                                                                                                                       R;Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N. Genomics 5, 527-534, 1989
                                                                                                                                                                                                                                                                                                                                                                                                testis-specific protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 29-Sep-1999
C;Accession: A33329
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R; IOZZO, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D. Genomics 14, 845-851, 1992
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A; Residues: 21-22, 'X', 24-37 <PE2>
A; Experimental source: brain
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A; Molecule type: mRNA
A; Residues: 1725, 'V', ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: J02814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2160 NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2109 NPC-----LNGGTCYPTETSYVCTCVPGYSGDQCELDFDECHSNPCRNGATCVDGF 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2256 STLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2211 RLQGAHLTSILSHEEQ----MFVNRV-----GHDYQ----WIGLNDKMFEHDFRWTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 EHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 -RFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 NPCRMSCQNHGRLNISTCH------CHCPPGYTGRYCQV------RCSLQCVHG- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,1727-2409 <KRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%;
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Pred. No. 1.1e-06;
""Fmatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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A; Molecule type: nucleic acid
A; Residues: 1-3562 <SHI>
A; Cross-references: GB:D15542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A; Cross-references: GB:D15542; NID:g391644
A; Cross-references: GB:D15425; NID:g391644
A; Cross-references: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
C:Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
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A;Accession: A47171
A;Status: preliminary
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F;3296-3327/Domain: E-fyp homology <EGF>
F;3334-3454/Domain: C-fyp lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>
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3400 RDFRWTDGSPLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTY 3452
                                                                                                                                                                     3355 WDTAERECRLQGAHLTSILSHEEQ----VFVNRI------GHDYQ----WIGLNDKMFE 3399
                                                                                                                                                                                                                                                                                                                                      3302 RNGATCIDGL---NTFTCLCLPSYIGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRT 3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 MSTDPTLWST-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 LKTKCQATC-----LCEDKIH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 CFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 VWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                            380 DSFRWATGEHQAFTSFAFGQPDNHGLYWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRY 439
                                                                                                                                                                                                                                                 320 YYRARMKCORKGGVLAQIKSOKVODILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 GGLCEVP-RNPCRMS-CQNHGRLNISTCH-----CHCPPGYTGRYCQV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IVNKHNELRRSVNPTGSDILKMEWSIQATTNAQKWANKCILEHSSKDDRKINIRCGENLY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPS-----LASG---- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKST--PYQQGTPCASCPNN--- 195
                                                                                                                                                                                                                                                                                                                                                                                                                           RCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 191; DB 2; Length 25.1%; Pred. No. 4e-06; 25.1%; Pred. No. 4e-06; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 193.5; DB 2; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VIQSWYNENEDFVYGVG-AKPNSAVGHYTQL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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A;Molecule type: mRNA
A;Residues: 1-1643 <SCH>
A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 273, 15758-15764, 1998
A,Title: Versican V2 is a major extracellular matrix component of the mature bovine b A;Reference number: Z17954; MUID:98288320; PMID:9624174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      versican precursor, splice form v2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: brain C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T14274
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                                                                                                                              Дb
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                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
Search completed: December 29, 2002, Job time: 55 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.5%;
Best Local Similarity 26.0%;
Matches 61; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3453 TCK 3455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1343 NPC-----LNGGTCYPTETSYVCTCVPGYSGDRCELDFDECHSNPCRNGATCIDGF 1393
                                                                                                                              1490 STLQYENWRPNQPDS----FFSTG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 1537
                                                                                                                                                                                                                                                                                                                                                                                      1394 NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC 1444
                                                                                                                                                                                                                                                        1445 RLQGAHLTSILSHEEQ----MFVNRV-----GHDYQ----WIGLNDKMFEHDFRWTDG 1489
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                                                                                                                                                                                                                                                                                                                    328 QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 NPCRMSCQNHGRLNISTCH-----CHCPPGYTGRYCQV-----RCSLQCVHG- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 -RFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKC 327
                                                                                                                                                                                         EHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Mismatches
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                                       02:26:41
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                             196
189.5
185
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1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/2

3: /cgn2_6/ptodata/2

4: /cgn2_6/ptodata/2

5: /cgn2_6/ptodata/2

6: /cgn2_6/ptodata/2
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2529
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              MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS
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Copyright (c) 1993 - 2002 Compus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                              Length DB
         US-08-840-062-5
US-08-614-935-28
US-09-130-287-224B-97
US-07-857-224B-98
US-07-857-224B-99
US-08-614-935-6
US-08-614-935-7
US-08-614-935-7
US-09-130-287-7
US-09-130-287-24B-100
US-09-257-583-13
US-07-857-224B-101
US-08-148-101
US-08-148-101
US-08-148-101
US-08-148-101
US-08-148-101
US-08-148-101
US-08-148-101
US-08-148-101
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US-09-199-887-1
US-08-773-368-3
US-09-199-887-3
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US-09-199-887-4
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Patent No. 518
Sequence 5, A
Sequence 28,
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              99, Appl
10, Appl
6, Appli
6, Appli
7, Appli
7, Appli
105, App
1105, App
1107, Appl
1107, Appl
1107, Appl
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1107, Appl
1108, Appl
1109, Appl
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28, Appl
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97, Appl
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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28
166	. 166	166	168	168	168.5	169	169	171	171	171	171	171	171	171	171	171	171
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US-09-130-287-2	US-08-614-935-2	US-08-419-414-9	US-09-199-887-6	US-08-773-368-6	PCT-US95-03747-2	US-09-130-287-1	US-08-614-935-1	US-09-350-600-45	US-08-971-217-45	US-08-455-736-45	US-08-456-240-45	US-08-456-262-45	US-08-457-364-45	US-08-454-876-45	US-08-455-244-45	US-08-455-416-45	US-08-456-265A-45
Sequence 2, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 45, Appl	•	Sequence 45, Appl	•	Sequence 45, Appl	`	`	`	`	`

ALIGNMENT

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RESULT 1
US-08-773-368-1
                                                                    US-08-773-368-1
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                  Query Match
Best Local
 Matches
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                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                         LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: 21P: 943
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                               TELEX:
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                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
 73;
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                    Similarity
                                                                                                                                                          amino acid
                                                                                                                                                                           270 amino acids
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Conservative
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                  10.6%; Score 267; DB 2; 31.5%; Pred. No. 3.6e-16;
 28; Mismatches
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                                 Length 270;
 Indels
 52;
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                                                                                                         Query Match
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                                                                         Matches
                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS: LENGTH: 270 amino acids
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-----GYHCKNSLCEPIGSP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
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11 LLPLLLLVATT------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57
                   13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                         Local Similarity
                                                                                                                                                             CLONE:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/199,887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV-----EV 123
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                                                                       Conservative
                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                            single
                                                                  10.6%; Score 267; DB 3; I
31.5%; Pred. No. 3.6e-16;
31.5%; o. Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                      PF-0186 US
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                                                                                                    Length 270;
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US-08-773-368-3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08773368 Patent No. 5856130
                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 847722
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-----GYHCKNSLCEPIGSP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162
     81
                            94 PSLASGLWRTLQVGWNMQLLPAGLASFYEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                                                                                                     47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP-----T 93
                                                                    21 EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH
                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
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     PNFTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWDEELAAFAKAYA-------RQXRXGHNKERGRRGENLFAITDEGMDVPLA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                           Similarity
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3174 Porter Drive
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Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                         415-845-4166
                                                                                                                                           Conservative
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--LGENIWTGSVPIFSVSSAITNWYDEIQDYNFKTRICKK--VCGHYTQV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                single
                                                                                                                                                         9.2%;
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                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF-0186 US
                                                                                                                                                         Score 232; DB 2;
Pred. No. 3.7e-13;
                                                                                                                                           Mismatches
                                                                                                                                                                         Length 219;
                                                                                                                                         Indels
                                                                                                                                         32;
                                                                                                                                     Gaps
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154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC

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US-08-773-368-4; Sequence 4, Application US/08773368
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                                           RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: GOLI, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 847722
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                                                                                                     132
                                                                                                                                       154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                 94 PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                             PNFTS-----LGENIWTGSVPIFSVSSAITNWYDEIQDYNEKTRICKK--VCGHYTQV 131
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                                                                                                                                                                                                                                                       EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 80
                                                                                                     VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                   9.2%; Score 232; DB 3; 32.4%; Pred. No. 3.7e-13;
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                                                                                                                                                                                                                                                                                                                                   28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   Length 219;
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                                                                                                     --WPYKRGATCSAC 185
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                                                                                                                                                           RESULT 6
US-09-199-887-4
                                                                                                                        ; Sequence 4, Application US/09199887; Patent No. 6071874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
               GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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CTTY: Palo Alto
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                    154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
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ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                 47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP------T 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                   VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 195
                                                                                                                                                                                                                                                                                                                                                                             EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 90
                                                                                                                                                                                                                                                                                                      PNFTS-----LGENIWTGSVPIFSVSSAITNWYDEIQDYDFKTRICKK--VCGHYTQV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 amino acids
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%; Pred. No. 5.9e-13;
27; Mismatches 62
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                                                                                                                                                                                                                                           Patent No. 5648465
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Sequence 49, Application US/08340428B Patent No. 5648465
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                                                                                                                                                                                         APPLICANT: RAUCH, Uwe APPLICANT: MARGOLIS, Renee K.
COMPUTER READABLE FORM:
                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                      TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
                                                                                                                                                                                                                          APPLICANT: MARGOLIS, Richard U.
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LIBRARY: GenBank
CLONE: 1030053
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NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                           142
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                                                                                                                                                                                                                                                                                                                                                                                                     154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
                                                                STREET: 419 Seven
                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP------T 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 POI
CITY: Palo Alto
                                                       STATE:
                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/199,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                         PNFTS-----LGENIWTGSVPIFSVSSAITNWYDEIQDYDFKTRICKK--VCGHYTQV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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                                                   D.C.
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                                                                                    419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                 U.S.A.
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                                                                                                      Browdy and Neimark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 231; DB 3; Length 266; 32.4%; Pred. No. 5.9e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
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RESULT 8
5180808-2
; Patent No.
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                                                                                                                                                                                                                                                                                  APPLICANT: RUOSLAHTI, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
ANTIBODIES, AND METHODS OF DETECTING THE SAME
                                                                                                                                                                               SEQ ID NO:2
                                             Matches
                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116 DNF-----FAGGEDCVVMVAHENGRWNDVPCNYNLPYVCK 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1071 EEHKFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1015 PSYGGNLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSP 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
230 NPCRMSCQNHGRLNISTCH-----CHCPPGYTGRYCQV------RCSLQCVHG- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 DNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AFVCAYSPGGNWEVNGKTIIPYKKGAWCS--LCTASVSGCFKAWDHAGGLCEVPRNPCRM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 KVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 ASVSSGEPTRLWDI-PSTLIPVSLGLDESDLKVVAESPGLEGFWEEVASGQEDPTDPCEN 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 IGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 SCONHG---RLNISTCHCHCPPGYTGRYCQV----RCSLQCVHGRFREEECS---CVCD 283
                                                                                                                                                                                                  APPLICATION NUMBER: US/
FILING DATE: 27-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    LENGTH: 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/922,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPCLHGGTCRTNGTMYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVNGFICLCL 1014
                                           ol Similarity
63; Conserv
                                                                                                                                                                                                                                                                                                                                                                               5180808
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                                           Conservative
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                                      7.8%; Score 196; DB 6; 1
26.8%; Pred. No. 1.5e-08;
tive 27; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.8%;
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24.8%; Pred. No. 2.4e-10;
ive 34; Mismatches 134
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                                                                                  Length 2409;
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-- rocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LASI APPLICANT: WU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2256 STLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2211 RLQGAHLTSILSHEEQ----MFVNRV-----GHDYQ----WIGLNDKMFEHDFRWTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2160 NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC
                                                                                                                                                             180 CA-----YSPGGNWEVNGK----TI------IPYKKGAWCSLCTASVSGC 214
                                                                                                                                                                                                    491 SHAVVPEGADKGCRKGWKRHGFYCYLIGSTLSTFTDANHTCTNEKAYLTTVEDRYEQAFL 550
                                                                                                                                                                                                                                             135 SHA-----AGECARNATCTH--YTQLVWATSSQLGCGRHLCS---AGQTAIE-----AFV 179
275 EEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGD------CFMV----SSEADTYY 321
                                                                                215 FKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFR 274
                                                                                                                      551 TSLVGLRPEKYFWTGLSDVQNKGTFRWTVDEQVQFTHWNADMPGRKAG----CVAMKTGV 606
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1455 ami
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPC-----LNGGTCYPTETSYVCTCVPGYSGDQCELDFDECHSNPCRNGATCVDGF 2159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1455 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                Linear
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                                                                                                                                                                                                                                                                                       7.5%; score 189.5; DB 3; 23.3%; Pred. No. 3e-08; tive 45; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                  Length 1455;
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GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IM
TITLE OF INVENTION: AN
                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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HYPOTHETICAL:
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                 107 GWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRH 166
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                                                                              51 LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
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New Jersey
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                                                                                                                          7.3%; Score 185; DB 1; Length 151; 30.5%; Pred. No. 3.7e-09; tive 28; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILLING DATE: 11-MAR-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
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120 YCPNQDSLKYYYVCQYCPAGN-NMNRKN-TPYQQ 151
                                167 LCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKK 200
                                                                                                            107 GWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRH 166
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STREET: 411 Hackensack Ave, (
STREET: Floor
                                                                       61 GENL-YMSSDPTSWSSAIQSWYDEILDFVYGVGPKSPNAVVGHYTQLVWYSTYQVGCGIA 119
                                                                                                                                                                                  51 LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQV 106
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les 47; Conser
                                                                                                                                                                                                                                                                                                                      ORGANISM:
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                                                                                                                                                 IVNKHNELRKAVSPPASNMLKMEWSREVTTNAQRWANKCTLQHSDPEDRKTS----TRC 60
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30.5%; Pred. No. 3.7e-09;
tive 28; Mismatches 67;
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                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 47; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
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112 CNNGWWFIS---CNYDPVGNW 129
                                                                                                                                                                                                                                                                                                             PAGES: >c.
                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                   52 LSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQ----ARAALCGIPTPSLASGLWRTLQVG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0 CLASSIFICATION:
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FILING DATE: 03/25/92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                    CSAGQTAIEAFVCAYSPGGNW 188
                                                                                                              WNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHL 167
                                                                                                                                                  LAVHNDARAQV-----GVGPMSWDANLASRAQNYANSRAGDCNL----IHSGAGENLAKG 58
                                                                       -----GGDFTGRAAVQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRAR 111
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: Carr, J. P.
: Klessig, D. F.
: Klessig, D. F.
: Isolation and nucleotide sequence of cDNA clones for the pathogenesis related proteins of Nicotiniana tabacum induced by TMV infection.
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                                                                                                                                                                                                                        7.2%; Score 182.5; DB 2
33.3%; Pred. No. 5.3e-09;
tive 17; Mismatches 54
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                                                                                                                                                                                                                                                               DB 2;
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US-07-857-224B-98
                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   AUTHORS: Cutt, J. M. AUTHORS: Dixon, D. C. AUTHORS: Dixon, D. C. AUTHORS: Carr, J. P. AUTHORS: Klessig, D. F. AUTHORS: Klessig, D. F. TITLE: Isolation and nucleotide sequence of cDNA clones for the TITLE: pathogenesis related proteins of Nicotiniana tabacum induced by TMV infertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: Pathogenesis related protein, Table 16 Row 2 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
112 CNNGWWFIS---CNYDPVGNW 129
                                                                                                     108 WNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                  168 CSAGQTAIEAFVCAYSPGGNW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
                                                                59 -----GGDFTGRAAVQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRAR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                              52 LSLHNRLRSWYQPPAADMRRLDWSDSLAQLAQ----ARAALCGIPTPSLASGLWRTLQVG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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OPERATING SYSTEM: MacInto:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Switzerland ZIP: (note: this is an international post code) CH-8092
                                                                                                                                                                                                                                                     ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                           LAVHNDARAQV-----GVGPMSWDANLASRAQNYANSRAGDCNL----IHSGAGENLAKG 58
                                                                                                                                                                                                                                47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum
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                                                                                                                                                                                                                    7.2%; Score 182.5; DB 2; Length 135; 33.3%; Pred. No. 5.3e-09; vative 17; Mismatches 54; Indels 23
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US-07-857-224B-99

; Sequence 10, Application US/08419414
; Patent No. 5753787

US-08-419-414-10

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RESULT 14

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                               112 CNNGWWFIS---CNYDPVGNW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Lycopersicon esculentum FEATURE: Pathogenesis related protein; PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                 108 WNMQLLPAGLASFYEVYSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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ADDRESSEE: Steven A. Benner
                                                                                  168 CSAGQTAIEAFVCAYSPGGNW 188
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                                                                                                               59 -----GGDFTGRAAVQLWVSERPDYNYATNQCVGGKMCGHYTQVVWRNSVRLGCGRAR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                             PAGES: 9861
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                   VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
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CITY: Zurich
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(note: this is an international post code) CH-8092
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Dixon, D. C.
Carr, J. P.
Klessig, D. F.
Klessig, D. F.
Isolation and nucleotide sequence of cDNA clones for the
Isolation and nucleotide sequence of Nicotiniana tabacum induced by TMV
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                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Research
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                                                                                                                                                                                                                                                                                                 DB 2; Length 135;
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APPLICANT: Hotez, Peter J.
APPLICANT: Jones, Brian F.
APPLICANT: Jones, Brian F.
APPLICANT: Hotez, Deter J.
APPLICANT: Hotez, Peter J.
APPLICANT: Hotez, Patan F.
CORRESPONDENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
Search completed: December 29, 2002, 02:27:28 Job time : 39 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
ORIGINAL SOURCE:
; ORGANISM: Pollstes annulatis
US-08-419-414-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YU113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8795
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTECHIEF TYPE: Profess
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                             149 HYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKK 200
                                                                                                157 HYTQMVWGKTKEIGCGSLKYMENNMQNHYLICNYGPAGNY--LGQ--LPYTK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
                                                                                                                                                                                                                                                                                       41 EEKKLIVSEHNRFRQKVAQGLETRGNPGPQPAASDMNDLVWNDELAHIAQVWASQCQF-- 98
                                                                                                                                                                                                                                                                                                                                                                                Match 7.1%; Score 180.5; DB 1; Length 205; Local Similarity 30.8%; Pred. No. 1.4e-08; es 53; Conservative 24; Mismatches 70; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                             25;
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94 PSLASGLWRT---LOVGWNMQLL-PAGLASFVEVVSLWFAEGQRYSHAAGECARN-ATCT 148 99 --LVHDKCRNTAKYPVGQNIAYAGGSNLPDVVSLIKLWENEVKDFNYNTGITKQNFAKIG 156 Gaps 7;